

## SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

### Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

### STAFF USE ONLY

Date completed: 05-29-03  
Searcher: Beverly 24994  
Terminal time: 20 40  
Elapsed time: \_\_\_\_\_  
CPU time: \_\_\_\_\_  
Total time: 60  
Number of Searches: \_\_\_\_\_  
Number of Databases: 1

#### Search Site

\_\_\_\_\_ STIC  
\_\_\_\_\_ CM-1  
\_\_\_\_\_ Pre-S

#### Type of Search

\_\_\_\_\_ N.A. Sequence  
\_\_\_\_\_ A.A. Sequence  
\_\_\_\_\_ Structure  
\_\_\_\_\_ Bibliographic

#### Vendors

\_\_\_\_\_ IG Suite  
\_\_\_\_\_ STN  
\_\_\_\_\_ Dialog  
\_\_\_\_\_ APS  
\_\_\_\_\_ Geninfo  
\_\_\_\_\_ SDC  
\_\_\_\_\_ DARC/Questel  
✓ Other CGN

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:30:20 ; Search time 29.333 Seconds  
(without alignments)  
99.938 Million cell updates/sec

Title: US-09-147-362a-2

Sequence: 1 LLSIMGCRGLVCTSYQWNET 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 13350620 residues

Number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A: Geneseq\_101002.\*

1:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
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3:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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19:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SID82/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
21:	/SID82/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
22:	/SID82/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
23:	/SID82/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	100.0	22	19	AAW80460
2	112	96.1	22	19	AAW80460
3	112	96.1	22	19	AAW80460
4	119	93.7	22	19	AAW80469
5	119	93.7	32	19	AAW80471
6	118	92.9	22	19	AAW80461
7	118	92.9	32	19	AAW80461
8	116	91.3	113	20	AAV05555
9	116	91.3	113	20	AAV05555
10	116	91.3	215	20	AAV09499

11	116	91.3	215	20	AAV05983	Recombinant pCO-8P
12	116	91.3	215	21	AAV77374	HIV-1 Group O env
13	116	91.3	245	20	AAV05472	Recombinant pCO-9P
14	116	91.3	245	21	AAV77369	Recombinant pCO-9P
15	116	91.3	281	20	AAV09507	HIV-1 Group O env
16	116	91.3	373	20	AAV09495	HIV-1 Group O env
17	116	91.3	373	20	AAV09500	Recombinant pCO-11
18	116	91.3	460	20	AAV05950	HIV-1 Group O env
19	116	91.3	460	20	AAV05984	HIV-1 Group O env
20	116	91.3	460	21	AAV77375	HIV-1 Group O env
21	116	91.3	468	20	AAV09504	HIV-1 Group O env
22	116	91.3	468	20	AAV09504	HIV-1 Group O env
23	116	91.3	490	20	AAV06978	Recombinant pCO-9C
24	116	91.3	490	21	AAV77370	HIV-1 Group O env
25	116	91.3	526	20	AAV09505	HIV-1 Group O env
26	116	91.3	526	20	AAV09505	HIV-1 Group O env
27	116	91.3	618	20	AAV06980	Recombinant pCO-11
28	116	91.3	618	21	AAV77372	HIV-1 Group O env
29	116	91.3	706	20	AAV09503	HIV-1 Group O env
30	116	91.3	715	20	AAV05625	HIV-1 Group O env
31	116	91.3	715	20	AAV05625	HIV-1 Group O env
32	116	91.3	735	20	AAV09501	HIV-1 Group O env
33	116	91.3	873	20	AAV09501	HIV-1 Group O env
34	116	91.3	873	20	AAV09501	HIV-1 Group O env
35	116	91.3	873	20	AAV09501	HIV-1 Group O env
36	115	90.2	104	17	AAW80245	HIV-1 Group O env
37	115	90.2	104	17	AAW80245	HIV-1 Group O env
38	114	89.8	32	19	AAW80469	Peptide derived fr
39	113	89.0	22	19	AAW80462	Peptide derived fr
40	113	89.0	113	20	AAV05559	HIV-1 Group O env
41	113	89.0	116	17	AAV05555	HIV-1 Group O env
42	113	89.0	116	17	AAV05555	HIV-1 Group O env
43	112	88.2	113	20	AAV05546	HIV-1 Group O env
44	112	88.2	117	20	AAV05548	HIV-1 Group O env
45	112	88.2	117	20	AAV05548	HIV-1 Group O env

ALIGNMENTS

RESULT 1  
ID AAW80460 standard; peptide: 22 AA.  
AC AAW80460;  
DX 28-JUN-1999 (first entry)  
DT Peptide derived from a conserved sequence of group O human HIV.  
FM Group O human immune deficiency virus; HIV; detection; infection.  
OS Synthetic.  
OS Immune deficiency virus.  
KW W09845323-A1.  
XX 15-OCT-1998.  
XX 06-APR-1998; 98WO-FR00691.  
XX 24-FEB-1998; 98FR-0002212.  
XX 09-APR-1997; 97FR-0004356.  
(SNF) PASTEUR SANOFT DIAGNOSTICS SA.  
Chenebaux DMB, Deligneau JFR, Gabelle SJX, Rieunier FY.  
WPI: 1998-583190/49.  
New synthetic peptide(s) - useful for, e.g. detecting infection by human immune deficiency virus of group O

PS Claim 6; Page 42; 55pp; French.

XX  
XX  
CC AAM80459-74 represent synthetic peptides (either linear or cyclized by  
CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
CC connected around short highly conserved sequences present in isolates  
CC of group O human immune deficiency virus (HIV). The peptides are  
CC useful as immunological reagents for detecting infection by group O  
CC human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 100.0%; Score 127; DB 19; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCTSYVOMNET 22  
DB 1 LLSLMGCRGLVCTSYVOMNET 22

LT 2

AAM80465  
AAM80465 standard; peptide; 22 AA.

XX AAM80465;

XX 28-JAN-1999 (first entry)

XX Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus; HIV; detection; infection.

XX Synthetic.  
XX Immune deficiency virus.

XX MO9845323-A1.

XX 15-OCT-1998.

XX 06-APR-1998; 98MO-FR00691.

XX 24-FEB-1998; 98FR-0002212.

XX 09-APR-1997; 97FR-0004356.

XX (SNP) PASTEUR SANOFI DIAGNOSTICS SA.

XX Cheneboux DMG, Delagrange JPH, Gabelle SJX, Rieunier FY;

XX WPI; 1998-583190/49.

PF New synthetic peptide(s) - useful for, e.g. detecting infection by  
PF human immune deficiency virus of group O

XX Claim 6; Page 43; 55pp; French.

XX AAM80459-74 represent synthetic peptides (either linear or cyclized by  
XX Cys-Cys disulphide bonds). The peptides represent variable sequences  
XX connected around short highly conserved sequences present in isolates  
XX of group O human immune deficiency virus (HIV). The peptides are  
XX useful as immunological reagents for detecting infection by group O  
XX human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 96.1%; Score 123; DB 19; Length 22;  
Best Local Similarity 95.5%; Pred. No. 8.3e-10;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCTSYVOMNET 22  
DB 1 LLSLMGCRGLVCTSYVOMNET 22

RESULT 3

XX AAM80466 standard; peptide; 22 AA.

XX AAM80466;

XX 28-JAN-1999 (first entry)

XX Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus; HIV; detection; infection.

XX Synthetic.  
XX Immune deficiency virus.

XX MO9845323-A1.

XX 15-OCT-1998.

XX 06-APR-1998; 98MO-FR00691.

XX 24-FEB-1998; 98FR-0002212.

XX 09-APR-1997; 97FR-0004356.

XX (SNP) PASTEUR SANOFI DIAGNOSTICS SA.

XX Cheneboux DMG, Delagrange JPH, Gabelle SJX, Rieunier FY;

XX WPI; 1998-583190/49.

PF New synthetic peptide(s) - useful for, e.g. detecting infection by  
PF human immune deficiency virus of group O

XX Claim 6; Page 43; 55pp; French.

XX AAM80459-74 represent synthetic peptides (either linear or cyclized by  
XX Cys-Cys disulphide bonds). The peptides represent variable sequences  
XX connected around short highly conserved sequences present in isolates  
XX of group O human immune deficiency virus (HIV). The peptides are  
XX useful as immunological reagents for detecting infection by group O  
XX human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 95.3%; Score 121; DB 19; Length 22;  
Best Local Similarity 95.5%; Pred. No. 1.1e-09;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSLMGCRGLVCTSYVOMNET 22  
DB 1 LLSLMGCRGLVCTSYVOMNET 22

RESULT 4

XX AAM80459 standard; peptide; 22 AA.

XX AAM80459;

XX 28-JAN-1999 (first entry)

XX Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus; HIV; detection; infection.

XX Synthetic.  
XX Immune deficiency virus.

XX MO9845323-A1.

XX 15-OCT-1998.

XX 06-APR-1998; 98MO-FR00691.



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XX 24-FEB-1998; 98FR-0002212.
PR 09-APR-1997; 97FR-0004356.
XX (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
PA Cheneboux DMB, Delagneau JFH, Gadelle SXH, Riennier FY.
PI WPI; 1998-583190/49.
XX
PT New synthetic peptide(s) - useful for, e.g. detecting infection by
PT human immune deficiency virus of group O
XX
XX Claim 6; Page 42; 55pp; French.
XX
XX AA06459-74 represent synthetic peptides (either linear or cyclised by
XX Cys-Cys disulphide bonds). The peptides represent variable sequences
XX connected around short highly conserved sequences present in isolates
XX of group O human immune deficiency virus (HIV). The peptides are
XX useful as immunological reagents for detecting infection by group O
XX human immune deficiency virus (HIV).
XX
XX Sequence 22 AA:
XX
XX Query Match 93.7%; Score 119; DB 19; Length 22;
XX Best Local Similarity 90.9%; Pred. No. 2.1e-09;
XX Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX Db 1 L1LSWCGRGRGLVCTSYVQNNET 22
XX 1 L1LSWCGRGRGLVCTSYVQNNET 22
XX
XX RESULT 5
XX AA06471
XX ID AA06471 standard; peptide; 32 AA.
XX
XX AA06471;
XX
XX DT 28-JAN-1999 (first entry)
XX
XX Peptide derived from a conserved sequence of group O human HIV.
XX
XX Group O human immune deficiency virus; HIV; detection; infection.
XX
XX Synthetic.
XX
XX Immune deficiency virus.
XX
XX MO9845323-AL.
XX
XX 15-OCT-1998. 98MO-FR00691.
XX
XX 06-APR-1998; 98FR-0002212.
XX
XX 24-FEB-1998; 98FR-0002212.
XX
XX 09-APR-1997; 97FR-0004356.
XX
XX (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
XX
XX Cheneboux DMB, Delagneau JFH, Gadelle SXH, Riennier FY.
XX
XX WPI; 1998-583190/49.
XX
XX New synthetic peptide(s) - useful for, e.g. detecting infection by
XX human immune deficiency virus of group O
XX
XX Claim 6; Page 44; 55pp; French.
XX
XX AA06459-74 represent synthetic peptides (either linear or cyclised by
XX Cys-Cys disulphide bonds). The peptides represent variable sequences
XX connected around short highly conserved sequences present in isolates
XX of group O human immune deficiency virus (HIV). The peptides are
XX useful as immunological reagents for detecting infection by group O

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CC human immune deficiency virus (HIV).
XX
XX Sequence 32 AA:
XX
XX Query Match 93.7%; Score 119; DB 19; Length 32;
XX Best Local Similarity 90.9%; Pred. No. 3e-09;
XX Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX Db 1 L1LSWCGRGRGLVCTSYVQNNET 22
XX 1 L1LSWCGRGRGLVCTSYVQNNET 22
XX
XX RESULT 6
XX AA06461
XX ID AA06461 standard; peptide; 22 AA.
XX
XX AA06461;
XX
XX 28-JAN-1999 (first entry)
XX
XX Peptide derived from a conserved sequence of group O human HIV.
XX
XX Group O human immune deficiency virus; HIV; detection; infection.
XX
XX Synthetic.
XX
XX Immune deficiency virus.
XX
XX MO9845323-AL.
XX
XX 15-OCT-1998.
XX
XX 06-APR-1998; 98MO-FR00691.
XX
XX 24-FEB-1998; 98FR-0002212.
XX
XX 09-APR-1997; 97FR-0004356.
XX
XX (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
XX
XX Cheneboux DMB, Delagneau JFH, Gadelle SXH, Riennier FY.
XX
XX WPI; 1998-583190/49.
XX
XX New synthetic peptide(s) - useful for, e.g. detecting infection by
XX human immune deficiency virus of group O
XX
XX Claim 6; Page 42; 55pp; French.
XX
XX AA06459-74 represent synthetic peptides (either linear or cyclised by
XX Cys-Cys disulphide bonds). The peptides represent variable sequences
XX connected around short highly conserved sequences present in isolates
XX of group O human immune deficiency virus (HIV). The peptides are
XX useful as immunological reagents for detecting infection by group O
XX human immune deficiency virus (HIV).
XX
XX Sequence 22 AA:
XX
XX Query Match 92.9%; Score 118; DB 19; Length 22;
XX Best Local Similarity 90.9%; Pred. No. 2.9e-09;
XX Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX Db 1 L1LSWCGRGRGLVCTSYVQNNET 22
XX 1 L1LSWCGRGRGLVCTSYVQNNET 22
XX
XX RESULT 7
XX AA06470
XX ID AA06470 standard; peptide; 32 AA.
XX
XX AA06470;
XX
XX DT 28-JAN-1999 (first entry)

```

XX Peptide derived from a conserved sequence of group O human HIV.  
 XX Group O human immune deficiency virus; HIV; detection; infection.  
 XX Synthetic.  
 XX Immune deficiency virus.  
 XX MO9845323-A1.  
 XX 15-OCT-1998.  
 XX 06-APR-1998; 98MO-FR00691.  
 XX 24-FEB-1998; 98EP-0002212.  
 XX 09-APR-1997; 97EP-0004356.  
 XX (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.  
 XX Cheneboux DMB, Delagneau JFH, Gabelle STX, Rieunier FY;  
 XX MPI; 1998-583390/49.  
 XX New synthetic peptide(6) - useful for, e.g. detecting infection by  
 XX human immune deficiency virus of group O  
 XX Claim 6; Page 44; 55pp; French.  
 XX AA980459-74 represent synthetic peptides (either linear or cyclized by  
 XX Cys-Cys disulphide bonds). The peptides represent variable  
 XX connected around short highly conserved sequences present in isolates  
 XX of group O human immune deficiency virus (HIV). The peptides are  
 XX human immune deficiency virus (HIV).  
 XX Sequence 32 AA;  
 XX  
 XX Query Match 92.9%; Score 118; DB 19; Length 32;  
 XX Best Local Similarity 86.4%; Pred. No. 4.1e-09;  
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 LISTMCKGRRLCYTSSVQNNMT 22  
 XX DB 11 LINTMCKGRRLCYTSSVQNNMT 32  
 XX  
 XX RESULT 8  
 XX AA773373  
 XX AA705565  
 XX AA705565 standard; Protein; 113 AA.  
 XX AA705565;  
 XX 19-JUL-1999 (first entry)  
 XX HIV-1 group O isolate MP539-PBMC gp41 antigen.  
 XX HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;  
 XX vaccine; diagnosis; AIDS.  
 XX Human immunodeficiency virus type 1.  
 XX Key Location/Qualifiers  
 XX Misc-difference 65 /note= "encoded by MMW"  
 XX Misc-difference 74 /note= "encoded by AVR"  
 XX Misc-difference 84 /note= "encoded by GAK"  
 XX Misc-difference 8/notes= "encoded by AQR"  
 XX MO9304011-A2.

PD 28-JAN-1999.  
 XX 20-JUL-1998; 98MO-EP04522.  
 XX 18-JUL-1997; 97EP-0870110.  
 XX (INNO-) INNOGENETICS NV.  
 XX Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;  
 XX MPI; 1999-132285/11.  
 XX N-PSDB; AA705565.  
 XX New isolated HIV-1 group O strains - used to produce  
 XX polynucleotides, antigens and antibodies for use in diagnosis and in  
 XX vaccines for prevention of HIV-1 infection  
 XX Claim 3; Fig 6; 162pp; English.  
 XX The present sequence is an antigen of the gp41 protein of HIV-1  
 XX group O (Outlier) strain MP539-PBMC, a Cameroon isolate. The  
 XX invention relates to new HIV-1 group O antigens (see AA705546-625),  
 XX and the use of these antigens, or nucleic acids encoding them (see  
 XX AA923147-80), in the diagnosis and prophylaxis of AIDS. They can be  
 XX differentiating different HIV-1 group O infection and for  
 XX vaccines that provide protective immunity against infection. In  
 XX particular against HIV-1 group O infection, complete at least one  
 XX HIV-1 type O antigen, a nucleic acid encoding such an antigen, a  
 XX virus-like particle comprising such an antigen, or an attenuated  
 XX HIV-1 group O strain. The invention also relates to new  
 XX neighbouring constructs.  
 XX Sequence 113 AA;  
 XX  
 XX Query Match 91.3%; Score 116; DB 20; Length 113;  
 XX Best Local Similarity 81.8%; Pred. No. 2.5e-08;  
 XX Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 LISTMCKGRRLCYTSSVQNNMT 22  
 XX DB 39 LINTMCKGRRLCYTSSVQNNMT 60  
 XX  
 XX RESULT 9  
 XX AA773373  
 XX ID AA77373 standard; Protein; 200 AA.  
 XX AA77373;  
 XX 22-MAY-2000 (first entry)  
 XX HIV-1 group O env gp120/gp41 pco-5 recombinant protein, SEQ ID NO:36.  
 XX HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;  
 XX immunodassay; positive control; affinity purification; therapeutic;  
 XX bacteriemia coli; antigen; synthetic gene construction; mutagen;  
 XX detection mutation.  
 XX Human immunodeficiency virus type 1 group O isolate HM112.  
 XX Synthetic.  
 XX MO200004383-A2.  
 XX 27-JAN-2000.  
 XX 09-JUL-1999; 99MO-US15469.  
 XX 14-JUL-1998; 98US-0115171.  
 XX (ABBO) ABBOTT LAB.





XX 15-AUG-1997; 97US-091824.  
 XX (ABRO ) ABBOTT LAB.  
 XX Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J,  
 XX WPI, 1999-190167/16.  
 XX N-PDB: AA556074.  
 XX  
 XX New isolated HIV-1 Group O env polypeptides - used for the  
 XX detection of anti-HIV antibodies and for the production of  
 XX antibodies for use in detection, purification and therapy  
 XX  
 XX Claim 16; Fig 7; 138pp; English.  
 XX  
 XX The present invention describes (A) an isolated HIV-1 Group O env  
 XX polypeptide. Also described are: (1) an isolated HIV-1 Group O env  
 XX polypeptide comprising an immunoreactive portion of a polypeptide as in  
 XX (A); (2) a polynucleotide (m) encoding a polypeptide as in (A); or (1)  
 XX (3) an antigen construct comprising a fusion of at least one HIV-1 Group O  
 XX polypeptide and at least one HIV-1 Group O env polypeptide with at  
 XX least one HIV-1 Group M env polypeptide; (5) an antigen construct  
 XX comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env  
 XX polypeptide, and at least one additional HIV-1 polypeptide; (6) an  
 XX antigen construct comprising a first HIV-2 env polypeptide fused to as  
 XX second HIV-2 env polypeptide; (7) a fusion of an antigen as in (3)-(6)  
 XX in (3)-(6); (8) an expression vector as in (8); and (10) an  
 XX immunoreactive kit for the detection of antibodies to HIV-1 comprising an  
 XX antigen construct as in (3)-(6). The antigen constructs can be used for  
 XX the detection of anti-HIV-1 antibodies in test samples. They can also be  
 XX used as immunogens to produce antibodies. The antibodies can be used to  
 XX purify HIV polypeptides, for therapy and for detection of HIV  
 XX polypeptides.  
 XX  
 XX Sequence 245 AA:  
 XX  
 XX Query Match 91.3%; Score 116; DB 20; Length 245;  
 XX Best Local Similarity 81.8%; Pred. No. 5.3e-08;  
 XX Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 LLSLMGCKGRRLVCTYSVNNET 22  
 XX DB 127 LLSLMGCKGRRLVCTYSVNNET 148  
 XX  
 XX RT 14  
 XX 6977  
 XX AA706977 standard; Protein: 245 AA.  
 XX AA706977;  
 XX 06-JUL-1999 (first entry)  
 XX Recombinant pCO-9PL protein.  
 XX HIV-1, HIV-2; immobilised capture reagent; capillary action; screening;  
 XX antibody; assay.  
 XX  
 XX Synthetic.  
 XX Human immunodeficiency virus type 1.  
 XX  
 XX Key 245 Location/Qualifiers  
 XX Protein /note="gp120 sequence"  
 XX Peptide /note="gp41 sequence"  
 XX  
 XX WC9309410-A2.  
 XX  
 XX 25-FEB-1999.

XX 07-AUG-1998; 98MO-US16506.  
 XX 15-AUG-1997; 97US-0912129.  
 XX (ABRO ) ABBOTT LAB.  
 XX Brennan CA, Devare SG, Golden AM, Hackett JR, Hickman RK;  
 XX Necklame EC, Vallari AS, Varilek V,  
 XX WPI, 1999-190224/16.  
 XX N-PDB: AA37185.  
 XX  
 XX New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -  
 XX can be used in field assay, requiring no electricity and less  
 XX specialised equipment  
 XX  
 XX Claim 1; Fig 7; 106pp; English.  
 XX  
 XX The invention relates to a rapid assay for simultaneous detection and  
 XX differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The  
 XX method comprises (a) contacting the sample with a strip containing at  
 XX least one immobilised capture reagent per analyte and on which the  
 XX sample moves from the proximal to the distal end by capillary action;  
 XX under conditions sufficient to form capture sites by detecting a visible  
 XX and (b) determining the capture reagent sites on the strip wherein the  
 XX capture reagent for HIV-1 group O comprises a polypeptide shown in  
 XX AA706977-80 and AA706981-84; and that for HIV-2 comprises a  
 XX polypeptide shown in AA706981-84; and that for HIV-1 group M comprises a  
 XX polypeptide shown in AA706981-84. The invention is used to screen patients  
 XX for antibodies to HIV-1 types O and M, and HIV-2. The method will be  
 XX particularly useful where the invention provides a screening method  
 XX which is faster and requires less equipment than prior art methods. The  
 XX present sequence represents a amino acid sequence of the recombinant  
 XX pCO-9PL recombinant protein which acts as a capture reagent for HIV-1  
 XX group O.  
 XX  
 XX Sequence 245 AA:  
 XX  
 XX Query Match 91.3%; Score 116; DB 20; Length 245;  
 XX Best Local Similarity 81.8%; Pred. No. 5.3e-08;  
 XX Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 LLSLMGCKGRRLVCTYSVNNET 22  
 XX DB 127 LLSLMGCKGRRLVCTYSVNNET 148  
 XX  
 XX RESULT 15  
 XX AA77369  
 XX ID AA77369 standard; Protein: 245 AA.  
 XX AA77369;  
 XX 22-MAY-2000 (first entry)  
 XX HIV-1 group O pCO-9PL-encoded truncated env gp41 protein, SEQ ID NO:48.  
 XX HIV-1 group O; env; gp120, gp41, gp130; monoclonal antibody;  
 XX immunoreactive; positive; antigen; synthetic gene construction; mutagen;  
 XX detection mutation.  
 XX  
 XX Synthetic.  
 XX Human immunodeficiency virus type 1 group O isolate HAM112.  
 XX  
 XX Key 245 Location/Qualifiers  
 XX Protein /note="gp120 sequence"  
 XX Peptide /note="gp41 sequence"  
 XX  
 XX WC200004383-A2.  
 XX  
 XX 27-JAN-2000.  
 XX  
 XX 09-JUL-1999; 99MO-US15469.



GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: May 29, 2003, 10:33:36 / Search time 9.95238 Seconds  
(without alignments)  
65,040 Million cell updates/sec

Title: US-09-147-362a-2  
Perfect score: 127  
Sequence: 1 ULSTMGRGRVRCVSYQNNR 22  
Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing filter 45 eliminates

Database: Issued Patents AA\*

- 1: /cgn2\_6/p/odata1/1/aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/p/odata1/1/aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/p/odata1/1/aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/p/odata1/1/aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/p/odata1/1/aa/6C\_COMB.pep.\*
- 6: /cgn2\_6/p/odata1/1/aa/6D\_COMB.pep.\*
- 7: /cgn2\_6/p/odata1/1/aa/6E\_COMB.pep.\*
- 8: /cgn2\_6/p/odata1/1/aa/6F\_COMB.pep.\*
- 9: /cgn2\_6/p/odata1/1/aa/6G\_COMB.pep.\*
- 10: /cgn2\_6/p/odata1/1/aa/6H\_COMB.pep.\*
- 11: /cgn2\_6/p/odata1/1/aa/6I\_COMB.pep.\*
- 12: /cgn2\_6/p/odata1/1/aa/6J\_COMB.pep.\*
- 13: /cgn2\_6/p/odata1/1/aa/6K\_COMB.pep.\*
- 14: /cgn2\_6/p/odata1/1/aa/6L\_COMB.pep.\*
- 15: /cgn2\_6/p/odata1/1/aa/6M\_COMB.pep.\*
- 16: /cgn2\_6/p/odata1/1/aa/6N\_COMB.pep.\*
- 17: /cgn2\_6/p/odata1/1/aa/6O\_COMB.pep.\*
- 18: /cgn2\_6/p/odata1/1/aa/6P\_COMB.pep.\*
- 19: /cgn2\_6/p/odata1/1/aa/6Q\_COMB.pep.\*
- 20: /cgn2\_6/p/odata1/1/aa/6R\_COMB.pep.\*
- 21: /cgn2\_6/p/odata1/1/aa/6S\_COMB.pep.\*
- 22: /cgn2\_6/p/odata1/1/aa/6T\_COMB.pep.\*
- 23: /cgn2\_6/p/odata1/1/aa/6U\_COMB.pep.\*
- 24: /cgn2\_6/p/odata1/1/aa/6V\_COMB.pep.\*
- 25: /cgn2\_6/p/odata1/1/aa/6W\_COMB.pep.\*
- 26: /cgn2\_6/p/odata1/1/aa/6X\_COMB.pep.\*
- 27: /cgn2\_6/p/odata1/1/aa/6Y\_COMB.pep.\*
- 28: /cgn2\_6/p/odata1/1/aa/6Z\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	91.3	215	2	US-08-912-1299-58
2	116	91.3	245	2	US-08-912-1299-58
3	116	91.3	373	2	US-08-912-1299-58
4	116	91.3	460	2	US-08-912-1299-58
5	116	91.3	618	2	US-08-912-1299-58
6	116	91.3	873	2	US-08-912-1299-58
7	116	91.3	37	4	US-08-817-441-94
8	115	90.6	104	4	US-08-817-441-94
9	115	90.6	356	1	US-08-602-713-12
10	113	89.0	355	1	US-08-817-441-94
11	113	89.0	355	1	US-08-817-441-94
12	112	88.2	200	4	US-08-965-056-104
13	112	88.2	23	4	US-08-894-699-39
14	111	87.4	40	4	US-08-894-699-39
15	111	87.4	40	4	US-08-894-699-39
16	111	87.4	40	4	US-08-894-699-39
17	111	87.4	41	4	US-08-894-699-39
18	111	87.4	41	4	US-08-894-699-39
19	110	86.6	40	3	US-08-894-699-41
20	110	86.6	40	3	US-08-894-699-41
21	110	86.6	40	3	US-08-894-699-41
22	110	86.6	40	4	US-09-444-410-41
23	110	86.6	40	4	US-09-444-410-41
24	109	85.8	40	4	US-08-894-699-37
25	109	85.8	40	4	US-08-894-699-37
26	108	85.0	40	4	US-09-444-410-40
27	108	85.0	40	4	US-09-444-410-40

28	107	84.3	23	4	US-08-433-428D-68	Sequence 68, App1
29	107	84.3	33	4	US-08-433-428D-1	Sequence 1, App1
30	107	84.3	33	4	US-08-433-428D-15	Sequence 15, App1
31	107	84.3	42	3	US-08-894-699-66	Sequence 66, App1
32	107	84.3	42	3	US-08-894-699-66	Sequence 66, App1
33	107	84.3	33	4	US-09-433-428D-5	Sequence 5, App1
34	106	83.5	33	4	US-09-433-428D-5	Sequence 5, App1
35	106	83.5	33	4	US-09-433-428D-14	Sequence 14, App1
36	106	83.5	33	4	US-09-433-428D-29	Sequence 29, App1
37	106	83.5	35	4	US-08-817-441-71	Sequence 71, App1
38	106	83.5	35	4	US-08-817-441-71	Sequence 71, App1
39	106	83.5	35	4	US-08-817-441-90	Sequence 90, App1
40	106	83.5	35	4	US-08-817-441-90	Sequence 90, App1
41	106	83.5	35	4	US-08-817-441-102	Sequence 102, App1
42	105	82.7	24	4	US-08-817-441-34	Sequence 34, App1
43	105	82.7	33	4	US-08-433-428D-10	Sequence 10, App1
44	105	82.7	33	4	US-08-433-428D-10	Sequence 10, App1
45	105	82.7	33	4	US-09-433-428D-19	Sequence 19, App1

## ALIGNMENTS

RESULT 1  
US-08-912-1299-58  
Sequence 58, App1 Application US/089121299  
Patent No. 5922533  
GENERAL INFORMATION:  
APPLICANT: VALIARI, ANDRUZEILA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: HICKMAN, ROBERT K. JR.  
APPLICANT: MATTHEW, VINCENT A. JR.  
APPLICANT: WATSON, ROBERT A.  
APPLICANT: GOLDEN, ALAN M.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEVAE, SUSHIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION OF  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESS: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
OPERATING SYSTEM: MS-DOS (Windows 95)  
SOFTWARE: Microsoft Word (ASCII format output)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912.1299  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 436  
PRIORITY NUMBER: 2176  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckerts, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109, US-01  
TELECOMMUNICATIONS INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
INFORMATION FOR SEO ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 215 amino acids  
TYPE: amino acids  
DEPENDENCY: single  
TOPOLOGY: linear  
US-08-912-1299-58

Query Match 91.3%; Score 116; DB 2; Length 215;  
Best Local Similarity 81.8%; Pred. No. 7, 8e-10;  
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LISTMCGRNLCTSVNMNET 22  
DB 127 LHMWCKGRNLCTSVNMNET 148

## RESULT 2

US-08-912-129A-48  
Patent No. 5922533

## GENERAL INFORMATION:

APPLICANT: VALLEART, ANADRUZELA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: HICKMAN, ROBERT K.  
APPLICANT: WARTER, VINCENT A. JR.  
APPLICANT: NECKLANS, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN N.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEVARA, SUSHIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESS: Abbott Laboratories  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500

## COMPUTER READABLE FORM:

OPERATING SYSTEM: MS-DOS (Windows 95)  
SOFTWARE: Microsoft Word (ASCII format output)  
CURRENT APPLICATION DATA:  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 436  
PRIORITY APPLICATION: 436  
PRIORITY APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckers, Andreas M.  
REGISTRATION NUMBER: 32,652  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623

## INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:  
LENGTH: 245 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-912-129A-48

Query Match 91.3%; Score 116; DB 2; Length 245;  
Best Local Similarity 81.8%; Pred. No. 9e-10;  
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LISTMCGRNLCTSVNMNET 22  
DB 127 LHMWCKGRNLCTSVNMNET 148

RESULT 3  
US-08-912-129A-52  
Sequence 52, Application US/08912129A  
Patent No. 5922533

GENERAL INFORMATION:  
APPLICANT: VALLEART, ANADRUZELA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: HICKMAN, ROBERT K.  
APPLICANT: WARTER, VINCENT A. JR.  
APPLICANT: NECKLANS, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN N.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEVARA, SUSHIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESS: Abbott Laboratories  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500

## COMPUTER READABLE FORM:

OPERATING SYSTEM: MS-DOS (Windows 95)  
SOFTWARE: Microsoft Word (ASCII format output)  
CURRENT APPLICATION DATA:  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 436  
PRIORITY APPLICATION: 436  
PRIORITY APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckers, Andreas M.  
REGISTRATION NUMBER: 32,652  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623

## INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:  
LENGTH: 373 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-912-129A-52

Query Match 91.3%; Score 116; DB 2; Length 373;  
Best Local Similarity 81.8%; Pred. No. 1.4e-09;  
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LISTMCGRNLCTSVNMNET 22  
DB 127 LHMWCKGRNLCTSVNMNET 148

## RESULT 4

US-08-912-129A-60  
Patent No. 5922533

## GENERAL INFORMATION:

APPLICANT: VALLEART, ANADRUZELA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: HICKMAN, ROBERT K.  
APPLICANT: WARTER, VINCENT A. JR.  
APPLICANT: NECKLANS, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN N.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEVARA, SUSHIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESS: Abbott Laboratories



STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM: 5 inch diskette, 1.44 MB  
OPERATING SYSTEM: MS-DOS (Windows 95)  
SOFTWARE: Microsoft Word (ASCII format output)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912.129A  
FILING DATE: 15-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckert, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109 US. 01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 460 amino acids  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-912-129A-50  
Query Match 81.3%; Score 116; DB 2; Length 460;  
Best Local Similarity 81.8%; Pred. No. 1.9e-09;  
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
DB 372 LNLWCKGRRLICVTYSVMNET 393  
CY 1 LLSLWCKGRRLICVTYSVMNET 22  
US-08-912-129A-50  
RESULT 5  
Sequence 50, Application US/08912129A  
Patent No. 5922533  
GENERAL INFORMATION:  
APPLICANT: VALLARI, ANANDRUELA S.  
APPLICANT: HACKETT, ROBERT K.  
APPLICANT: VIKRAM, VINCENT A. JR.  
APPLICANT: NECKLAMS, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN M.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEVADE, SUSHIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION  
OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
OPERATING SYSTEM: MS-DOS (Windows 95)  
SOFTWARE: Microsoft Word (ASCII format output)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912.129A  
FILING DATE: 15-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckert, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109 US. 01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 54:

CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckert, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109 US. 01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 490 amino acids  
TYPE: amino acid  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-912-129A-50  
Query Match 91.3%; Score 116; DB 2; Length 490;  
Best Local Similarity 81.8%; Pred. No. 1.9e-09;  
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
DB 372 LNLWCKGRRLICVTYSVMNET 393  
CY 1 LLSLWCKGRRLICVTYSVMNET 22  
US-08-912-129A-54  
RESULT 6  
Sequence 54, Application US/08912129A  
Patent No. 5922533  
GENERAL INFORMATION:  
APPLICANT: VALLARI, ANANDRUELA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: VIKRAM, VINCENT A. JR.  
APPLICANT: NECKLAMS, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN M.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEVADE, SUSHIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION  
OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
OPERATING SYSTEM: MS-DOS (Windows 95)  
SOFTWARE: Microsoft Word (ASCII format output)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912.129A  
FILING DATE: 15-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckert, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109 US. 01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 54:

Thu May 29 15:24:55 2003

us-09-147-362a-2.ra1

Page 4

SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-912-129A-54

Query Match 91.3% Score 116, DB 2; Length 618;  
Best Local Similarity 81.8%; Pred. No. 2, 4e-09;  
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L15LMGCRGALVCTSYVNMET 22  
Db 372 L15LMGCRGALVCTSYVNMET 393

RESULT 7  
US-08-912-129A-61

Sequence 61; Application US/08912129A

GENERAL INFORMATION:

APPLICANT: VALLARI, ANARHUZELA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: HICKMAN, ROBERT K.  
APPLICANT: VARTER, VINCENT A. JR.  
APPLICANT: NECKLAWS, ELIZABETH A.  
APPLICANT: BRENNAN, KATHLEEN M.  
APPLICANT: DEVARIE, SUSHIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESSES:  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Microsoft Word (ASCII format output)  
CURRENT APPLICATION DATA:  
FILING DATE: 15-AUG-1997  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NO.: 816  
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:  
NAME: Danckert, Andreas M.  
REGISTRATION NUMBER: 32,652  
TELECOMMUNICATIONS INFORMATION:  
TELEPHONE: 847-397-9803  
TELEFAX: 847-938-2623  
TELEX:

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:  
LENGTH: 873 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-912-129A-61

Query Match 91.3% Score 116, DB 2; Length 873;  
Best Local Similarity 81.8%; Pred. No. 3, 4e-09;  
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L15LMGCRGALVCTSYVNMET 22

Db 601 L15LMGCRGALVCTSYVNMET 622

RESULT 8  
US-08-817-441-94

Sequence 94; Application US/08817441

GENERAL INFORMATION:

APPLICANT: CHARNEAU, PIERRE  
APPLICANT: CLAVEL, FRANCOISE  
APPLICANT: SPYRIDIS, ANTONIS  
APPLICANT: OULIANT, JOCELYNE  
APPLICANT: GUERARD, DENISE  
APPLICANT: MONTAGNER, LUC  
APPLICANT: DONTON DE SAINT-MARTIN, JACQUELINE  
APPLICANT: COHEN, JACQUES  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE I OR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESSES:  
STREET: 1300 I Street, N.W.  
CITY: Washington  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Microsoft Word 6.0, version 1.1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 11-JUL-1997  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NO.: 95/01391  
APPLICATION NUMBER: PCT/FR 95/01391

FILING DATE: 20-OCT-1995

APPLICATION NUMBER: FR 9412554

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 9502526

FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Danckert, Andreas M.  
REGISTRATION NUMBER: 32,652  
TELECOMMUNICATIONS INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4000

INFORMATION FOR SEQ ID NO: 94:

SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-817-441-94

Query Match 90.6% Score 115, DB 4; Length 37;  
Best Local Similarity 81.8%; Pred. No. 1, 7e-10;  
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 L15LMGCRGALVCTSYVNMET 22  
Db 14 L15LMGCRGALVCTSYVNMET 35

RESULT 9  
US-08-817-441-100

Sequence 100; Application US/08817441



PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 06/602,713  
 FILING DATE: 16-FEBRUARY-1996  
 APPLICATION NUMBER: DB 195 05 262  
 ATTORNEY/AGENT INFORMATION:  
 NAME: / HAST, INFORMATION:  
 REGISTRATION NUMBER: 30 946  
 REFERENCE/DOCKET NUMBER: LEHR 203  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 688-1884  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 356 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: Protein  
 PDB ENTRY TYPE: Internal  
 8-989-931-12

Query Match 89.0%; Score 113; DB 4; Length 356;  
 Best Local Similarity 77.3%; Pred. No. 3,7e-09;  
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

1 LISTMCGRRLVCTSVQVNET 22  
 DB 322 LHMCKGKRLVCTSVQVNET 343

RESULT 12  
 US-08-817-441-86  
 Patent No. 6,392,411 Application US/08817441  
 GENERAL INFORMATION:  
 APPLICANT: CHAINEAU, PIERRE  
 APPLICANT: CLAVEL, FRANCOISE  
 APPLICANT: BORMAN, ANDREW  
 APPLICANT: GUILLENT, CAROLINE  
 APPLICANT: GUYARD, DENISE  
 APPLICANT: MONTEAU, PIERRE  
 APPLICANT: DONON DE SAINT-MARTIN, JACQUELINE  
 APPLICANT: COHEN, JAOUS  
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR  
 NUMBER OF SEQUENCES: 103  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dunne LLP  
 STREET: 1100 I Street, N.W.  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/817,441  
 FILING DATE: 16-FEB-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/FR 95/01391  
 FILING DATE: 20-OCT-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 9412554  
 FILING DATE: 20-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 9505526  
 FILING DATE: 03-MAR-1995  
 ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 01260, 6005-00000  
 TELECOMMUNICATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 86:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 37 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-817-441-86

Query Match 88.2%; Score 112; DB 4; Length 37;  
 Best Local Similarity 81.8%; Pred. No. 4,7e-10;  
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 LISTMCGRRLVCTSVQVNET 22  
 DB 14 LHMCKGKRLVCTSVQVNET 35

RESULT 13  
 US-08-965-056-104  
 Sequence 104, Application US/08965056  
 Patent No. 6,271,198  
 GENERAL INFORMATION:  
 APPLICANT: Andrew C. Balaisted  
 APPLICANT: J. Kevin Justice  
 APPLICANT: Joseph J. Duda  
 APPLICANT: J. Christopher Phelan  
 APPLICANT: Melissa A. Strovanski  
 APPLICANT: James A. Wells  
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
 NUMBER OF SEQUENCES: 113  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch 1.44 Mb floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Winpatin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/965,056  
 FILING DATE: 15-SEP-1997  
 CLASSIFICATION: 520 6271198-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Torchia, PhD., Timothy E.  
 REGISTRATION NUMBER: 36,700  
 REFERENCE/DOCKET NUMBER: P100582  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/4528674  
 TELEFAX: 650/4528674  
 INFORMATION FOR SEQ ID NO: 104:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 200 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-965-056-104

Query Match 88.2%; Score 112; DB 4; Length 200;  
 Best Local Similarity 81.8%; Pred. No. 2,8e-09;  
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 LISTMCGRRLVCTSVQVNET 22

Db 126 LISTGCKGRKALCYTSYVNNET 147

RESULT 14  
US-08-817-441-30

References: 30 Application US/08817441  
Patent No. 6139294

GENERAL INFORMATION:

APPLICANT: CHARNVAL, PIERRE  
APPLICANT: CLAVEL, FRANCOISE  
APPLICANT: BORMAN, ANDREW  
APPLICANT: OULIEN, CAROLINE  
APPLICANT: BORDON, DENIS  
APPLICANT: MONTAGNIER, ILC  
APPLICANT: DONJON DE SAINT-MARTIN, JACQUELINE  
APPLICANT: COHEN, JACQUES  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR  
TITLE OF INVENTION: SUBTYPE) ANTIGENS  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS: Henderson, Fairbow, Garrett &  
ADDRESS: Dunner, L.L.P.  
STREET: 1360 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3115  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/817,441  
APPLICATION NUMBER: 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR 95/00391  
FILING DATE: 20-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 9412554  
FILING DATE: 20-OCT-1994  
PRIOR APPLICATION DATA: FR 9502526  
FILING DATE: 03-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03460,6005-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: linear  
MOLCULE TYPE: peptide  
US-08-817-441-30

Query Match 87.4%; Score 111; DB 4; Length 23;  
Best Local Similarity 81.0%; Pred. No. 4e-10; 1; Indels 0; Gaps 0;  
Matches 17; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Cy 2 LISTGCKGRKALCYTSYVNNET 22  
1 LISTGCKGRKALCYTSYVNNET 21  
Db 1 LISTGCKGRKALCYTSYVNNET 21

RESULT 15  
US-08-894-699-39  
Sequence 39; Application US/08894699

Patent No. 6030769

GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: LAMONTAGNE, GILBERT  
APPLICANT: LOUSSET-ARAYA, IBETTISAM  
APPLICANT: LY, THOI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS: SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
STREET: FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/894,699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA: FR 95/02236  
APPLICATION NUMBER: 1997  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-2220  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: linear  
MOLCULE TYPE: peptide  
US-08-894-699-39

Query Match 87.4%; Score 111; DB 3; Length 40;  
Best Local Similarity 81.8%; Pred. No. 7.2e-10; 1; Indels 0; Gaps 0;  
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Cy 1 LISTGCKGRKALCYTSYVNNET 22  
1 LISTGCKGRKALCYTSYVNNET 40  
Db 19 LISTGCKGRKALCYTSYVNNET 40

Search completed: May 29, 2003, 10:41:27  
Job time : 10.9524 secs

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```

APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sunil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US 01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 48
LENGTH: 245
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-9PL
8-911-824-48

```

```

Query Match      91.3% Score 116; DB 1; Length 245;
Best Local Similarity 81.8% Pred. NO. 4,6e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
1 LLSMCKGRRLICVTSVMKNET 22
Db 127 LLMWCKGRRLICVTSVMKNET 148

```

```

RESULT 3
US-08-911-824-120
Sequence 120; Application US/08/911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sunil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US 01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 120
LENGTH: 281
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-15PL
US-08-911-824-120

```

```

Query Match      91.3% Score 116; DB 1; Length 281;
Best Local Similarity 81.8% Pred. NO. 5,2e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
1 LLSMCKGRRLICVTSVMKNET 22
Db 127 LLMWCKGRRLICVTSVMKNET 148

```

```

RESULT 4
US-08-911-824-52
Sequence 52; Application US/08/911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.

```

```

APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sunil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US 01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 52
LENGTH: 373
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-11PL
US-08-911-824-52

```

```

Query Match      91.3% Score 116; DB 1; Length 373;
Best Local Similarity 81.8% Pred. NO. 6,8e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
1 LLSMCKGRRLICVTSVMKNET 22
Db 127 LLMWCKGRRLICVTSVMKNET 148

```

```

RESULT 5
US-08-911-824-60
Sequence 60; Application US/08/911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sunil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US 01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 460
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-8CKS
US-08-911-824-60

```

```

Query Match      91.3% Score 116; DB 1; Length 460;
Best Local Similarity 81.8% Pred. NO. 8,2e-09;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
1 LLSMCKGRRLICVTSVMKNET 22
Db 372 LLMWCKGRRLICVTSVMKNET 193

```

```

RESULT 6
US-08-911-824-95
Sequence 95; Application US/08/911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie

```



APPLICANT: Golden, Alan M.  
 APPLICANT: Brennan, Catherine A.  
 APPLICANT: Hickman, Robert K.  
 APPLICANT: Devare, Sushil G.  
 TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
 FILE REFERENCE: 6165 US.O1  
 CURRENT APPLICATION NUMBER: US/08/911,824  
 CURRENT FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 121  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 488  
 TYPE: PRT  
 ORGANISM: Human Immunodeficiency Virus  
 FEATURE:  
 OTHER INFORMATION: Encodes recombinant protein pCO-14PL  
 US-08-911-824-95

Query Match 91.3% Score 116, DB 1, Length 488,  
 Best Local Similarity 81.8%, Pred. No. 8,7e-09,  
 Matches 18; Conservative 4; Mismatches 0; Indels 0;

QY 1 LLSLMGCRGRILCYTSVQNNET 22  
 DB 127 LLSLMGCRGRILCYTSVQNNET 148

RESULT 7  
 US-08-911-824-50  
 Sequence 50, Application US/08911824  
 Publication No. US20030004323A1  
 GENERAL INFORMATION:  
 APPLICANT: Abbott Laboratories  
 APPLICANT: Devare, Sushil G.  
 APPLICANT: Vasanuchi, Julie  
 APPLICANT: Golden, Alan M.  
 APPLICANT: Brennan, Catherine A.  
 APPLICANT: Hickman, Robert K.  
 APPLICANT: Devare, Sushil G.  
 TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
 FILE REFERENCE: 6165 US.O1  
 CURRENT APPLICATION NUMBER: US/08/911,824  
 CURRENT FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 121  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 50  
 LENGTH: 490  
 TYPE: PRT  
 ORGANISM: Human Immunodeficiency Virus  
 FEATURE:  
 OTHER INFORMATION: Encodes recombinant protein pCO-9CKS  
 US-08-911-824-50

Query Match 91.3% Score 116, DB 1, Length 490,  
 Best Local Similarity 81.8%, Pred. No. 8,7e-09,  
 Matches 18; Conservative 4; Mismatches 0; Indels 0;

QY 1 LLSLMGCRGRILCYTSVQNNET 22  
 DB 372 LLSLMGCRGRILCYTSVQNNET 393

RESULT 8  
 US-08-911-824-97  
 Sequence 97, Application US/08911824  
 Publication No. US20030004323A1  
 GENERAL INFORMATION:  
 APPLICANT: Abbott Laboratories  
 APPLICANT: Devare, John R., Jr.  
 APPLICANT: Vasanuchi, Julie  
 APPLICANT: Golden, Alan M.

APPLICANT: Brennan, Catherine A.  
 APPLICANT: Hickman, Robert K.  
 APPLICANT: Devare, Sushil G.  
 TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
 FILE REFERENCE: 6165 US.O1  
 CURRENT APPLICATION NUMBER: US/08/911,824  
 CURRENT FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 121  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 526  
 TYPE: PRT  
 ORGANISM: Human Immunodeficiency Virus  
 FEATURE:  
 OTHER INFORMATION: Encodes recombinant protein pCO-15CKS  
 US-08-911-824-97

Query Match 91.3% Score 116, DB 1, Length 526,  
 Best Local Similarity 81.8%, Pred. No. 9,3e-09,  
 Matches 18; Conservative 4; Mismatches 0; Indels 0;

QY 1 LLSLMGCRGRILCYTSVQNNET 22  
 DB 372 LLSLMGCRGRILCYTSVQNNET 393

RESULT 9  
 US-08-911-824-54  
 Sequence 54, Application US/08911824  
 Publication No. US20030004323A1  
 GENERAL INFORMATION:  
 APPLICANT: Abbott Laboratories  
 APPLICANT: Devare, Sushil G.  
 APPLICANT: Vasanuchi, Julie  
 APPLICANT: Golden, Alan M.  
 APPLICANT: Brennan, Catherine A.  
 APPLICANT: Hickman, Robert K.  
 APPLICANT: Devare, Sushil G.  
 TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
 FILE REFERENCE: 6165 US.O1  
 CURRENT APPLICATION NUMBER: US/08/911,824  
 CURRENT FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 121  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 54  
 LENGTH: 618  
 TYPE: PRT  
 ORGANISM: Human Immunodeficiency Virus  
 FEATURE:  
 OTHER INFORMATION: Encodes recombinant protein pCO-11CKS  
 US-08-911-824-54

Query Match 91.3% Score 116, DB 1, Length 618,  
 Best Local Similarity 81.8%, Pred. No. 9,3e-09,  
 Matches 18; Conservative 4; Mismatches 0; Indels 0;

QY 1 LLSLMGCRGRILCYTSVQNNET 22  
 DB 372 LLSLMGCRGRILCYTSVQNNET 393

RESULT 10  
 US-08-911-824-93  
 Sequence 93, Application US/08911824  
 Publication No. US20030004323A1  
 GENERAL INFORMATION:  
 APPLICANT: Abbott Laboratories  
 APPLICANT: Devare, John R., Jr.  
 APPLICANT: Vasanuchi, Julie  
 APPLICANT: Golden, Alan M.





Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSLMGCRGLVCTSVONNET 22  
 |||||:|||||:|||||  
 Db 14 LLSLMGCKGKLVCYTSVKNNRT 35  
 |||||:|||||:|||||

Search completed: May 29, 2003, 11:03:56  
 Job time : 20.0317 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:06 ; Search time 10.8254 Seconds

(without alignments)  
159,370 Million cell updates/sec

Title: US-09-147-362a-2

Perfect score: 127

Sequence: 1 L1SMCGRGNLYCVSYVNNET 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Result No. Score Match Length DB ID Description

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	115	90.6	104	2	SS2930	GP41 ENV protein -
2	112	88.2	104	2	AS3034	env polypeptide pr
3	106	83.5	877	2	S41937	env polypeptide pr
4	99	70.1	854	2	VCLJST	env polypeptide pr
5	86	67.7	358	2	S22002	env polypeptide pr
6	86	67.7	358	2	S22002	env polypeptide pr
7	85	66.9	358	2	S22000	env polypeptide pr
8	85	66.9	358	2	S70417	env polypeptide pr
9	84	66.1	443	2	C41621	env polypeptide pr
10	84	66.1	853	2	SS4384	env polypeptide pr
11	84	66.1	853	2	VCLJZR	env polypeptide pr
12	83	65.4	357	2	S22006	env polypeptide pr
13	83	65.4	357	2	S22004	env polypeptide pr
14	83	65.4	357	2	S22004	env polypeptide pr
15	83	65.4	357	2	S21992	env polypeptide pr
16	83	65.4	357	2	S21992	env polypeptide pr
17	83	65.4	358	2	S21998	env polypeptide pr
18	83	65.4	445	2	A41621	env polypeptide pr
19	83	65.4	445	2	A41621	env polypeptide pr
20	83	65.4	445	2	HA4061	env polypeptide pr
21	83	65.4	445	2	HA4061	env polypeptide pr
22	83	65.4	852	2	S13289	env polypeptide pr
23	83	65.4	852	2	VCLJZR	env polypeptide pr
24	83	65.4	852	2	T12016	env polypeptide pr
25	83	65.4	854	2	S13288	env polypeptide pr
26	83	65.4	855	2	VCLJNZ	env polypeptide pr
27	83	65.4	855	2	VCLJNZ	env polypeptide pr
28	83	65.4	856	2	VCLJNZ	env polypeptide pr
29	83	65.4	856	2	VCLJNZ	env polypeptide pr

## ALIGNMENTS

30	83	65.4	861	1	VCLJLV	env polypeptide pr
31	83	65.4	861	1	VCLJLV	env polypeptide pr
32	83	65.4	861	1	VCLJLV	env polypeptide pr
33	81	63.8	859	1	VCLJMN	env polypeptide pr
34	81	63.8	868	1	VCLJMN	env polypeptide pr
35	80	63.0	846	1	VCLJND	env polypeptide pr
36	77	60.6	729	1	VCLJRX	env polypeptide pr
37	77	60.6	861	1	VCLJRX	env polypeptide pr
38	76	59.8	866	2	S28084	env polypeptide pr
39	76	59.8	866	2	S28084	env polypeptide pr
40	74	58.3	851	2	T01572	env polypeptide pr
41	72.5	57.1	855	2	A45713	env polypeptide pr
42	68.5	53.9	859	2	VCLJST	env polypeptide pr
43	68.5	53.9	859	2	S24571	env polypeptide pr
44	68.5	53.9	885	2	S04322	env polypeptide pr
45	68.5	53.9	886	2	T11555	env polypeptide pr

## RESULT 1

GP41 ENV protein - human immunodeficiency virus type 1 (fragment)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Accession: S52930  
R:Comen, J.H.M.; Ouelard, D.; Philibert, F.; Chameret, S.; Tabary, T.; Montagnier, L.; de  
submitted to the EMBL Data Library, January 1995  
A:Description: A novel HIV-1 strain illustrates the diversity of the O group.  
A:Accession: S52930  
A:Status: preliminary  
A:Accession: S52930  
A:Status: preliminary  
A:Residues: 1-104 <CDS>  
A:Cross-references: EMBL:X64328; NID:G695526; PIDD:CA59066.1; PID:G695527  
C:Superfamily: type E retrovirus env polypeptide

Query Match 90.6%; Score 115; DB 2; Length 104;  
Best Local Similarity 81.8%; Pred. No. 1,36-09;

Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 45 L1SMCGRGNLYCVSYVNNET 22  
45 L1SMCGRGNLYCVSYVNNET 66

## RESULT 2

AS3034 polypeptide - human immunodeficiency virus type 1 (strain Ant70)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
C:Accession: AS3034  
R:Yarden Haesevelde, M.; Decourt, J.L.; De Leyer, R.J.; Vanderborcht, B.; van der Groen,  
J.; Virel, F.; 1986-1996, 1994  
A:Title: Genomic cloning and complete sequence analysis of a highly divergent African hu  
A:Accession: AS3034; M01D:9419849; PMID:8107220  
A:Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-863 <VAN>  
A:Cross-references: G8:102587  
C:Superfamily: type E retrovirus env polypeptide

Query Match 88.2%; Score 112; DB 2; Length 863;  
Best Local Similarity 81.8%; Pred. No. 2,26-08;

Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 594 L1SMCGRGNLYCVSYVNNET 22  
594 L1SMCGRGNLYCVSYVNNET 615



C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 12-Apr-1995  
 C/Accession: S22000  
 R/Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL data library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi  
 A:Accession: S22000  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1,358 <STR>  
 A:Cross-references: EMBL:X61351  
 C:Superfamily: type E retrovirus env polypeptin

Query Match 66.9% Score 85; DB 2; Length 358;  
 Best Local Similarity 65.0%; Pred. No. 8,46-05;  
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 LLSLMGCRGRVCTYSVQNN 20  
 P 94 LLSLMGCRGRVCTTVPMNS 113

RESULT 8  
 S70417  
 A:envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment  
 C/Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: patient 3B #sequence\_revision 25-Apr-1997 #text\_change 26-Aug-1999  
 C/Accession: S70417  
 R/Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70417  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1,358 <STR>  
 A:Cross-references: EMBL:X61351; NID:960184; PIDN:CAA43614.1; PID:960185  
 C:Superfamily: type E retrovirus env polypeptin

Query Match 66.9% Score 85; DB 2; Length 358;  
 Best Local Similarity 65.0%; Pred. No. 8,46-05;  
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 LLSLMGCRGRVCTYSVQNN 20  
 Db 94 LLSLMGCRGRVCTTVPMNS 113

RESULT 9  
 C/Date: 20-Feb-1995  
 A:envelope protein P - human immunodeficiency virus type 1 (fragment)  
 N:Alternate names: coat polypeptin  
 N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
 C/Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C/Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
 R/Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb  
 A:Reference number: A4621; MUID:92107924; PMID:1763038  
 A:Accession: C41621  
 A:Molecule type: DNA  
 A:Residues: 1,443 <STR>  
 A:Cross-references: GB:X61351; NID:9328631; PIDN:AAH03792.1; PID:9555015  
 A:Note: This virus was isolated from the mother's sexual partner  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polypeptin  
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
 F:1,251/Product: coat protein gp120 (fragment) #status predicted <GP2>  
 F:1252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>

F:423-443/Domain: transmembrane #status predicted <TM>  
 F:9,23,36,48,78,101,107,131,137,143,147,153,168,200,203,351,356,365,377/Binding site: ca  
 Query Match 66.1% Score 84; DB 2; Length 443;  
 Best Local Similarity 54.5%; Pred. No. 0.00014;  
 Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 LLSLMGCRGRVCTYSVQNN 22  
 Db 332 LLSLMGCRGRVCTTVPMNS 353

RESULT 10  
 S54384  
 A:envelope polypeptin - human immunodeficiency virus type 1  
 C/Species: human immunodeficiency virus type 1, HIV-1  
 C/Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999  
 A:Accession: S54384  
 R/Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL data library, July 1989  
 A:Reference number: S54377  
 A:Accession: S54384  
 A:Status: preliminary  
 A:Molecule type: genomic RNA  
 A:Residues: 1,853 <TM>; MUID:923937; PIDN:AAA45370.1; PID:9329385  
 C:Superfamily: type E retrovirus env polypeptin  
 C:Keywords: polypeptin

Query Match 66.1% Score 84; DB 2; Length 853;  
 Best Local Similarity 54.5%; Pred. No. 0.00025;  
 Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 LLSLMGCRGRVCTYSVQNN 22  
 Db 589 LLSLMGCRGRVCTTVPMNS 610

RESULT 11  
 VCA2CR  
 A:envelope protein precursor - human immunodeficiency virus Zr-6  
 N:Alternate names: coat polypeptin  
 C/Species: human immunodeficiency virus Zr-6  
 C/Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999  
 C/Accession: D26192  
 R/Srinivasan, A.; Anand, R.; Ranganathan, P.; Feorino, P.; Scholtenman, G.; Cu  
 Gene 52, 71-82, 1987  
 A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotid  
 A:Accession: D26192; MUID:87248097; PMID:3036660  
 A:Accession: D26192  
 A:Molecule type: DNA  
 A:Residues: 1,855 <STR>  
 A:Cross-references: GB:X03458; GB:MI3322; NID:9329398; PIDN:AAA45380.1; PID:9329403  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polypeptin  
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypept  
 F:1,139/Domain: signal sequence #status predicted <SIG>  
 F:20-850/Product: env polypeptin #status predicted <ENV>  
 F:501-855/Product: exterior membrane glycoprotein #status predicted <EXT>  
 F:87,129,140,145,154,158,169,199,236,243,264,276,291,297,333,340,355,366,392,398,404,  
 Query Match 66.1% Score 84; DB 1; Length 855;  
 Best Local Similarity 54.5%; Pred. No. 0.00025;  
 Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 LLSLMGCRGRVCTYSVQNN 22  
 Db 591 LLSLMGCRGRVCTTVPMNS 612

RESULT 12

522006  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)  
 C/Species: human immunodeficiency virus type 1, HIV-1  
 C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 A/Accession: S70420, S22006  
 A/Residues: 1-357 <STR>  
 A/Molecule type: DNA  
 A/Status: preliminary  
 A/Accession: S70420  
 A/Reference number: S70417, MUID:92144209, PMID:1736940  
 A/Note: submitted to the EMBL Data Library, July 1991  
 C/Superfamily: type E retrovirus env polypeptide

Query Match 65.4%; Score 83; DB 2; Length 357;  
 Best Local Similarity 60.0%; Pred. No. 0.00016;  
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 Oy 1 L1SMGCRGRLVCTVYVNN 20  
 Db 93 L1GIMGCSKILCTTAVPNN 112

RESULT 13  
 521994  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C/Species: human immunodeficiency virus type 1, HIV-1  
 A/Variety: isolate 278  
 C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 A/Accession: S21994, S70421  
 A/Residues: 1-357 <STR>  
 A/Molecule type: DNA  
 A/Status: preliminary  
 A/Accession: S21994  
 A/Reference number: S21990  
 A/Note: submitted to the EMBL Data Library, July 1991  
 C/Superfamily: type E retrovirus env polypeptide

Query Match 65.4%; Score 83; DB 2; Length 357;  
 Best Local Similarity 60.0%; Pred. No. 0.00016;  
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 Oy 1 L1SMGCRGRLVCTVYVNN 20  
 Db 93 L1GIMGCSKILCTTAVPNN 112

RESULT 14  
 522004  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C/Species: human immunodeficiency virus type 1, HIV-1  
 A/Variety: isolate 48  
 C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 A/Accession: S22004, S70419  
 A/Residues: 1-357 <STR>  
 A/Molecule type: DNA  
 A/Status: preliminary  
 A/Accession: S22004  
 A/Reference number: S21990

A/Accession: S22004  
 A/Residues: 1-357 <STR>  
 A/Molecule type: DNA  
 A/Status: preliminary  
 A/Accession: S22004  
 A/Reference number: S21990  
 A/Note: submitted to the EMBL Data Library, July 1991  
 C/Superfamily: type E retrovirus env polypeptide

Query Match 65.4%; Score 83; DB 2; Length 357;  
 Best Local Similarity 60.0%; Pred. No. 0.00016;  
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 Oy 1 L1SMGCRGRLVCTVYVNN 20  
 Db 93 L1GIMGCSKILCTTAVPNN 112

RESULT 15  
 521996  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
 C/Species: human immunodeficiency virus type 1, HIV-1  
 C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 A/Accession: S70422, S21996  
 A/Residues: 1-357 <STR>  
 A/Molecule type: DNA  
 A/Status: preliminary  
 A/Accession: S70422  
 A/Reference number: S70417, MUID:92144209, PMID:1736940  
 A/Note: submitted to the EMBL Data Library, July 1991  
 C/Superfamily: type E retrovirus env polypeptide

Query Match 65.4%; Score 83; DB 2; Length 357;  
 Best Local Similarity 60.0%; Pred. No. 0.00016;  
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 Oy 1 L1SMGCRGRLVCTVYVNN 20  
 Db 93 L1GIMGCSKILCTTAVPNN 112

Search completed: May 29, 2003, 10:40:23  
 Job time: 10.8254 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:31:50.1 Search time 5.4127 Seconds

(without alignments) 169,581 Million cell updates/sec

Title: US-09-147-362a-2

Sequence: 1 LSLMGCRRLVCYSQWNNR 22

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwIsprot 40.\*

Pepl. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	89	70.1	854	ENV_SIVC2	P17281 chimpanzee
2	84	66.1	852	ENV_HV12	P04580 human
3	83	65.4	843	ENV_HV12	P35961 human
4	83	65.4	847	ENV_HV12	P19550 human
5	83	65.4	847	ENV_HV12	P05880 human
6	83	65.4	851	ENV_HV12	P04580 human
7	83	65.4	851	ENV_HV12	P12488 human
8	83	65.4	852	ENV_HV12	P19550 human
9	83	65.4	852	ENV_HV12	P04580 human
10	83	65.4	852	ENV_HV12	P03376 human
11	83	65.4	852	ENV_HV12	P03376 human
12	83	65.4	852	ENV_HV12	P03376 human
13	83	65.4	852	ENV_HV12	P03376 human
14	83	65.4	852	ENV_HV12	P03376 human
15	83	65.4	852	ENV_HV12	P03376 human
16	83	65.4	852	ENV_HV12	P03376 human
17	83	65.4	852	ENV_HV12	P03376 human
18	83	65.4	852	ENV_HV12	P03376 human
19	83	65.4	852	ENV_HV12	P03376 human
20	83	65.4	852	ENV_HV12	P03376 human
21	83	65.4	852	ENV_HV12	P03376 human
22	83	65.4	852	ENV_HV12	P03376 human
23	83	65.4	852	ENV_HV12	P03376 human
24	83	65.4	852	ENV_HV12	P03376 human
25	83	65.4	852	ENV_HV12	P03376 human
26	83	65.4	852	ENV_HV12	P03376 human
27	83	65.4	852	ENV_HV12	P03376 human
28	83	65.4	852	ENV_HV12	P03376 human
29	83	65.4	852	ENV_HV12	P03376 human
30	83	65.4	852	ENV_HV12	P03376 human
31	83	65.4	852	ENV_HV12	P03376 human
32	83	65.4	852	ENV_HV12	P03376 human
33	83	65.4	852	ENV_HV12	P03376 human

## ALIGNMENTS

Result No.	Score	Match	Length	ID	Description
1	89	70.1	854	ENV_SIVC2	P17281 chimpanzee
2	84	66.1	852	ENV_HV12	P04580 human
3	83	65.4	843	ENV_HV12	P35961 human
4	83	65.4	847	ENV_HV12	P19550 human
5	83	65.4	847	ENV_HV12	P05880 human
6	83	65.4	851	ENV_HV12	P04580 human
7	83	65.4	851	ENV_HV12	P12488 human
8	83	65.4	852	ENV_HV12	P19550 human
9	83	65.4	852	ENV_HV12	P04580 human
10	83	65.4	852	ENV_HV12	P03376 human
11	83	65.4	852	ENV_HV12	P03376 human
12	83	65.4	852	ENV_HV12	P03376 human
13	83	65.4	852	ENV_HV12	P03376 human
14	83	65.4	852	ENV_HV12	P03376 human
15	83	65.4	852	ENV_HV12	P03376 human
16	83	65.4	852	ENV_HV12	P03376 human
17	83	65.4	852	ENV_HV12	P03376 human
18	83	65.4	852	ENV_HV12	P03376 human
19	83	65.4	852	ENV_HV12	P03376 human
20	83	65.4	852	ENV_HV12	P03376 human
21	83	65.4	852	ENV_HV12	P03376 human
22	83	65.4	852	ENV_HV12	P03376 human
23	83	65.4	852	ENV_HV12	P03376 human
24	83	65.4	852	ENV_HV12	P03376 human
25	83	65.4	852	ENV_HV12	P03376 human
26	83	65.4	852	ENV_HV12	P03376 human
27	83	65.4	852	ENV_HV12	P03376 human
28	83	65.4	852	ENV_HV12	P03376 human
29	83	65.4	852	ENV_HV12	P03376 human
30	83	65.4	852	ENV_HV12	P03376 human
31	83	65.4	852	ENV_HV12	P03376 human
32	83	65.4	852	ENV_HV12	P03376 human
33	83	65.4	852	ENV_HV12	P03376 human







	Query Match	Similarity	65.4%	Score	83	DB 1	Length	847
	Best Local	Similarity	60.0%	Pred.	No. 3.7e-05			
	Matches	12	Conservative	4	Mismatches	4	Indels	0
Cy			1	LISGWSGGKLCITTTTPVN	20			
Db			583	LISGWSGGKLCITTTTPVN	602			
 RESULT 7								
ENV_HV18B		STANDARD:		PRT:	851 AA.			
ID	ENV_HV18B							
AC	F04582							
DT	13-AUG-1987	(Rel.)	05	Created:				
DT	13-AUG-1987	(Rel.)	05	Last annotation update:				
DT	15-JUL-1999	(Rel.)	38	Last sequence update:				
DE	Envelope polypeptide gp160 precursor (Glycoprotein [gp11]).							
DE	Glycoprotein [gp120], Transmembrane glycoprotein (gp11).							
GN	ENV.							
OR	Human immunodeficiency virus type 1 (HR) isolate (HTV-1).							
OS	Viruses; Retrod viruses; Retroviridae; Lentivirus.							
XN	NCBI TaxId=11684;							

[illegible]



FT CAROBYD 385 385 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 393 393 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 397 397 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 401 401 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 405 405 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 442 442 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 457 457 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 607 607 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 612 612 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 613 613 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 812 812 N-LINKED (GLCNAC...) (POTENTIAL)  
 SO SEQUENCE 852 AA: 96663 MW: EEEHBE92C9910D CRG64;  
 Query Match 65.4%; Score 83; DB 1; Length 852;  
 Best Local Similarity 60.0%; Freq. No. 376-05;  
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 1 LLSIMCGRGLVCTSYQVN 20  
 588 LLSIMCGRGLVCTSYQVN 607  
 RESULT 10  
 ENV\_HVLA2 STANDARD; PRT: 853 AA.  
 AC P19551;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).  
 OS Human immunodeficiency virus type 1 (HIV-1).  
 OC Viruses; Retroviral; Retroviridae; Lentivirus.  
 NC NCB1\_TaxID:11704;  
 RN [1]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE=90117877; PubMed=169534;  
 RX Stevenson M., Haggerty S., Lamont C., Mann A.M., Meler C., "Enveloping and characterization of human immunodeficiency virus type 1 variants diminished in the ability to induce syncytium-independent cytolysis";  
 RT cytolysis";  
 RL J. Virol. 64:3792-3803 (1990).  
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 CC -----  
 CC EMBL: M35943; AAA44850.1;  
 CC  
 CC HIV: M35943; EMBL: M35943; ENV GP41.  
 CC InterPro: IPR000077; GP120.  
 CC Pfam: PF00517; GP120; 1.  
 DR Pfam: PF00517; GP120; 1.  
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.  
 KM SIGNAL.  
 FT CHAIN 31 30  
 FT DISULFID 510 509 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT DISULFID 518 508 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 119 203 BY SIMILARITY.  
 FT DISULFID 126 194 BY SIMILARITY.  
 FT DISULFID 131 157 BY SIMILARITY.  
 FT DISULFID 216 245 BY SIMILARITY.  
 FT DISULFID 226 237 BY SIMILARITY.  
 FT DISULFID 294 329 BY SIMILARITY.  
 FT DISULFID 376 443 BY SIMILARITY.

FT DISULFID 383 416 BY SIMILARITY.  
 FT CAROBYD 393 393 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 397 397 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 401 401 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 442 442 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 457 457 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 607 607 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 612 612 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 613 613 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CAROBYD 812 812 N-LINKED (GLCNAC...) (POTENTIAL)  
 SO SEQUENCE 853 AA: 96912 MW: 3377893B622AB CRG64;  
 Query Match 65.4%; Score 83; DB 1; Length 853;  
 Best Local Similarity 60.0%; Freq. No. 376-05;  
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 1 LLSIMCGRGLVCTSYQVN 20  
 590 LLSIMCGRGLVCTSYQVN 609  
 RESULT 11  
 ENV\_HVLA2 STANDARD; PRT: 855 AA.  
 AC P03378;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).  
 OS Human immunodeficiency virus type 1 (HIV-1).  
 OC Viruses; Retroviral; Retroviridae; Lentivirus.  
 NC NCB1\_TaxID:11685;  
 RN [1]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE=85090453; PubMed=257822;  
 RX Stevenson M., Brown S., Shear S., Gee W.M., Renard A., Randolph A., Levy J.A., Dina D., Luciw P.A., "Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2)";  
 RT Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2)";  
 RL Science 227:484-492 (1985).  
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 CC -----  
 CC EMBL: M02007; AA859882.1;  
 CC









Query Match 65.48; Score 83; DB 1; Length 856;  
 Best Local Similarity 60.08; Fred. No. 3.8e-05;  
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 LLSFWGCGSRGAVGYSYQNN 20  
 |||:|||||:|||||  
 Db 592 LIGIWGCGSKLICITTAAPWN 611

Search completed: May 29, 2003, 10:36:58  
 CDD time : 6.417 secs

**THIS PAGE BLANK (USPTO)**

GenScan version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:32:35 ; Search time 22.6984 Seconds  
(without alignments)  
199.707 Million cell updates/sec

Title: US-09-147-362a-2

Perfect score: 127

Sequence: 1 LISTMCGRCGRVCYTSYKNNET 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671560 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 671560

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP archaea.\*  
2: SP bacteria.\*  
3: SP fungi.\*  
4: SP plants.\*  
5: SP invertebrate.\*  
6: SP mammal.\*  
7: SP mhc.\*  
8: SP organelle.\*  
9: SP phage.\*  
10: SP plant.\*  
11: SP rodent.\*  
12: SP vertebrate.\*  
13: SP vertebrate.\*  
14: SP unclassified.\*  
15: SP virus.\*  
16: SP bacteriophage.\*  
17: SP archaea.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the highest score obtained. The score is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	119	91.7	209	15	Q91666 human immun
2	116	91.3	116	15	O40458 human immun
3	116	91.3	124	15	O91H07 human immun
4	116	91.3	126	15	O91H01 human immun
5	116	91.3	230	15	O91EB2 human immun
6	116	91.3	240	15	O91EB3 human immun
7	116	91.3	536	15	O91EB5 human immun
8	116	91.3	886	15	O807H1 human immun
9	116	91.3	900	15	O90R26 human immun
10	116	91.3	900	15	O90R26 human immun
11	115	90.6	104	15	O76163 human immun
12	115	90.6	216	15	O91EC7 human immun
13	115	90.6	535	15	O91EC2 human immun
14	114	89.8	123	15	O91H08 human immun
15	114	89.8	230	15	O91E29 human immun
16	114	89.8	239	15	O91E31 human immun

## ALIGNMENTS

17	114	89.8	229	15	O91E32 human immun
18	113	89.0	116	15	O40459 human immun
19	113	89.0	137	15	O91H05 human immun
20	113	89.0	172	15	O91EB3 human immun
21	113	89.0	177	15	O91EB0 human immun
22	113	89.0	208	15	O91EB3 human immun
23	113	89.0	227	15	O91EB9 human immun
24	113	89.0	234	15	O91E32 human immun
25	113	89.0	234	15	O91E32 human immun
26	113	89.0	416	15	O16547 human immun
27	113	89.0	502	15	O91E33 human immun
28	113	89.0	871	15	O57074 human immun
29	113	89.0	871	15	O80712 human immun
30	113	89.0	876	15	O807H3 human immun
31	113	89.0	113	15	O40456 human immun
32	112	88.2	114	15	O40456 human immun
33	112	88.2	118	15	O40451 human immun
34	112	88.2	213	15	O91E34 human immun
35	112	88.2	225	15	O91E34 human immun
36	112	88.2	234	15	O91E36 human immun
37	112	88.2	532	15	O91E36 human immun
38	112	88.2	545	15	O91E37 human immun
39	112	88.2	551	15	O91E37 human immun
40	112	88.2	551	15	O91E37 human immun
41	112	88.2	875	15	O90075 human immun
42	112	88.2	875	15	O90075 human immun
43	111	87.4	116	15	O11941 human immun
44	111	87.4	116	15	O40449 human immun
45	111	87.4	118	15	O40450 human immun

## RESULTS

1 Q91E66 PRELIMINARY; PRT; 209 AA.

AC Q91E66, 01-OCT-2000 (TEMBLrel), 15, Created)  
 DT 01-OCT-2000 (TEMBLrel), 15, Last sequence update)  
 DE 1-UDC-2000 (TEMBLrel), 15, Last annotation update)  
 GN 1-UDC-2000 (TEMBLrel), 15, Last annotation update)  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=89T107;  
 RA Deglenn C. Brum-Vezina F., Dormont D., Simon F.O.;  
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1."  
 RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AJ238862; CAB6300.1;  
 DR InterPro: IPR000318; Env\_Gp41.  
 DR Pfam: PF00517; Gp41\_1.  
 DR NCBI\_MolMap: 1  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 209 AA; 2416 MW; 91AC9B2B874803 CRC64;

Query Match 93.7%; Score 119; DB 15; Length 209;

Best Local Similarity 86.4%; Pred. No. 1,76-10; Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LISTMCGRCGRVCYTSYKNNET 22

Db 56 LISTMCGRCGRVCYTSYKNNET 77

RESULT 2

O40458 PRELIMINARY; PRT; 116 AA.



091E32 PRELIMINARY; PRT; 240 AA.  
 ID 091E32  
 AC 01-OCT-2000 (TRENBLER). 15. Created)  
 DT 01-OCT-2000 (TRENBLER). 15. Last sequence update)  
 DT 01-DEC-2001 (TRENBLER). 19. Last annotation update)  
 DE TM, GP41 (Fragment).  
 OS ENV.  
 GN Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NC NCBI\_TaxID=11676;  
 RN [1]\_TaxID=11676;  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=BCF11;  
 RA Rognes P., Robertson D., Souquiere S., Diamond F., Maucelere P.,  
 Delepierre C., Brun-Vezinet F., Dormont D., Simon P.O.,  
 "Phylogenetic analysis and subtyping of 47 HIV-1-group O isolates";  
 J. Virol. 75:1594-1596 (2001).  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 DR InterPro: IP0000328; Env\_GP41.  
 PF Pfam: PF00517; GP41; 1. \_Env\_GP41.  
 FT Transmembrane. 1  
 FT NON\_TER 1  
 FT TER 240  
 SQ SEQUENCE 240 AA; 27733 MW; 1E206E8D941A197 CRC64;  
 Query Match 91.3% Score 116; DB 15; Length 240;  
 Best Local Similarity 81.8%; Pred. No. 5,5e-10;  
 Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

01 LSLMCGRGLCYTSVQNNKT 22  
 Db 60 LSLMCGRGLCYTSVQNNKT 81

RESULT 7  
 091E35 PRELIMINARY; PRT; 536 AA.  
 ID 091E35  
 AC 01-OCT-2000 (TRENBLER). 15. Created)  
 DT 01-OCT-2000 (TRENBLER). 15. Last sequence update)  
 DT 01-DEC-2001 (TRENBLER). 19. Last annotation update)  
 DE ENV Polypeptide (Fragment).  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NC NCBI\_TaxID=11676;  
 RN [1]\_TaxID=11676;  
 RC SEQUENCE FROM N.A.  
 RP Rognes P., Robertson D., Diamond F., Souquiere S., Maucelere P.,  
 Delepierre C., Brun-Vezinet F., Dormont D.,  
 "HIV-1 group O phylogenetic analysis of C2-GP41 region";  
 J. Virol. 75:1594-1596 (2001).  
 RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ131062; CAB96233.1; InterPro: IP0000328; Env\_GP41.  
 DR InterPro: IP0000328; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
 FT NON\_TER 1  
 FT TER 536  
 SQ SEQUENCE 536 AA; 60419 MW; 0F531ABAFO8FE552 CRC64;  
 Query Match 91.3% Score 116; DB 15; Length 536;  
 Best Local Similarity 81.8%; Pred. No. 1,2e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

01 LSLMCGRGLCYTSVQNNKT 22  
 Db 361 LSLMCGRGLCYTSVQNNKT 382

RESULT 8  
 091E39 PRELIMINARY; PRT; 879 AA.  
 ID 091E39  
 AC 08O7H1  
 DT 01-NOV-1999 (TRENBLER). 12. Created)  
 DT 01-NOV-1999 (TRENBLER). 12. Last sequence update)  
 DT 01-DEC-2001 (TRENBLER). 19. Last annotation update)  
 DE GP150 precursor.  
 OS ENV.  
 GN Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NC NCBI\_TaxID=11676;  
 RN [1]\_TaxID=11676;  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=VI666;  
 RA MEDLINE=9223950; PubMed=10207543;  
 RA Janssens W., Heyndrickx L., Conder S., Williams B., Franssen K.,  
 Peeters M., Ndame P., Delaporte E., Van der Groen G.,  
 "Interpretation genetic variability of HIV-1 group O";  
 AIDS 13:41-48 (1999).  
 RT AIDS 13:41-48 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VI666;  
 RA MEDLINE=9642644; PubMed=8628748;  
 RA Baret J.B., Dittmann V., Georges Courbot M.C., Georges A.,  
 Bourgeois A., Samb B., Henzel D., Heyndrickx L., Franssen K.,  
 Van der Groen G., Larouz B., Mbé J.R.,  
 "Epidemiological and Molecular characteristics of HIV infection in  
 Gabon (1986 - 1994)";  
 AIDS 10:903-910 (1996).  
 RL MEDLINE=9351352; PubMed=878327.1;  
 DR InterPro: IP0000328; Env\_GP41.  
 DR Pfam: PF00517; GP41; 1.  
 DR Pfam: PF00517; GP120; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Signal; Transmembrane.  
 FT SIGNAL 1  
 FT CHAIN 30  
 FT CHAIN 528  
 FT CHAIN 130  
 FT CHAIN 164  
 FT CHAIN 302  
 FT CHAIN 395  
 FT CHAIN 458  
 FT CHAIN 525  
 SQ SEQUENCE 879 AA; BC4422ADDF1A3409 CRC64;  
 Query Match 91.3% Score 116; DB 15; Length 879;  
 Best Local Similarity 81.8%; Pred. No. 1,9e-09;  
 Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

01 LSLMCGRGLCYTSVQNNKT 22  
 Db 605 LSLMCGRGLCYTSVQNNKT 626

RESULT 9  
 08O7H1 PRELIMINARY; PRT; 880 AA.  
 ID 08O7H1  
 AC 08O7H1  
 DT 01-JUN-2002 (TRENBLER). 21. Created)  
 DT 01-JUN-2002 (TRENBLER). 21. Last sequence update)  
 DT 01-DEC-2001 (TRENBLER). 19. Last annotation update)  
 DE Envelope glycoprotein.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NC NCBI\_TaxID=11676;  
 RN [1]\_TaxID=11676;  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=96CMA407;  
 RX MEDLINE=21849375; PubMed=11860674;

Yamaguchi J., Vallari A.S., Swanson P., Devolle P., Kaptue L.,  
 RA Ngeop C., Zekeng L., Gurtler L.G., Delavay S.G., Brennan C.A.,  
 RT "Evaluation of HIV Type 1 Group O Isolates: Identification of Five  
 RT Phylogenetic Clusters."  
 RA AIDS Res. Hum. Retroviruses 18:269-282(2002).  
 RA Sequence 353820, AAL96872.1, F509J358E0301EE CRC64,  
 SO SEQUENCE 980 AA; 95764 MW; F509J358E0301EE CRC64;

Query Match 91.3%; Score 116; DB 15; Length 880;  
 Best Local Similarity 81.8%; Pred. No. 1.9e-09;  
 Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LISTMCGRGLVCYTSYONMET 22  
 Db 608 LISTMCGRGLVCYTSYONMET 629

## RESULT 10

09N028 PRELIMINARY; PRT; 900 AA.  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE ENV protein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 CO Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NC3 \_taxid=11676;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=97CA-MP645M/O;  
 MEDLINE=9370180; PubMed=10438826;  
 RA Pectere M., Liegeois P., Tortino N., Bourgeois A., Mound E.,  
 RA Gagne J., Sana E., Delaporte E., Sargoret S.,  
 RT "Characterization of a new active integrase W/O human  
 RT immunodeficiency virus type 1 recombinant isolated from a Cameroonian  
 RT patient."  
 RU J. Virol. 73:7368-7375(1999).  
 DR EMBL: AJ239083; CABS3242.1;  
 DR InterPro: IPR000328; ENV\_Gp41.  
 DR Pfam: PF00517; Gp41\_1.  
 DR Pfam: PF00517; Gp41\_1.  
 RA AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 900 AA; 109567 MW; FDB55726A357966 CRC64;

Query Match 91.3%; Score 116; DB 15; Length 900;  
 Best Local Similarity 86.4%; Pred. No. 2e-09; 1; Indels 0; Gaps 0;  
 Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 LISTMCGRGLVCYTSYONMET 22  
 Db 628 LISTMCGRGLVCYTSYONMET 649

## RESULT 11

076163 PRELIMINARY; PRT; 104 AA.  
 AC 076163;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE HIV-1 ENV (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 CO Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=VAD00R; Philbert F., Chamarat S., Tabary T.,  
 RA Chamarat S., Brun-Vezinet F., Montegier L., De Saint Martin C.,

"A novel HIV-1 O strain illustrates the diversity of the O group."  
 RT AIDS Res. Hum. Retroviruses 18:269-282(2002).  
 RA EMBL: X84328; CABS5066.1; ENV\_Gp41.  
 DR InterPro: IPR000328; ENV\_Gp41.  
 DR Pfam: PF00517; Gp41\_1.  
 GN Transmembrane.  
 FT NON\_TER  
 FT NON\_TER  
 SO SEQUENCE 104 AA; 10339 MW; D549218D0610067 CRC64;

Query Match 90.6%; Score 115; DB 15; Length 104;  
 Best Local Similarity 81.8%; Pred. No. 3.5e-10;  
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 LISTMCGRGLVCYTSYONMET 22  
 Db 45 LISTMCGRGLVCYTSYONMET 66

## RESULT 12

091EC7 PRELIMINARY; PRT; 216 AA.  
 DT 01-DEC-2000 (TREMBLrel. 15, Created)  
 DT 01-DEC-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Gp41 (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 CO Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NC3 \_taxid=11676;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BCF03;  
 RA Philippe M.,  
 RA "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
 RT AIDS Res. Hum. Retroviruses 18:269-282(2002).  
 DR EMBL: AJ161392; CABS624.1; ENV\_Gp41.  
 DR InterPro: IPR000328; ENV\_Gp41.  
 DR Pfam: PF00517; Gp41\_1.  
 GN Transmembrane.  
 FT NON\_TER  
 FT NON\_TER  
 SO SEQUENCE 216 AA; 23015 MW; 780C5F39C6697CC CRC64;  
 Query Match 90.6%; Score 115; DB 15; Length 216;  
 Best Local Similarity 86.4%; Pred. No. 7.1e-10;  
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 LISTMCGRGLVCYTSYONMET 22  
 Db 55 LISTMCGRGLVCYTSYONMET 76

## RESULT 13

091EF2 PRELIMINARY; PRT; 535 AA.  
 DT 01-DEC-2000 (TREMBLrel. 15, Created)  
 DT 01-DEC-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE ENV polypeptide (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 CO Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=BCF03;  
 RA Rogues P., Robertson D., Diamond F., Souquiere S., Mauleire P.,  
 RA Delpeche C., Brun-Vezinet F., Dormont D.,  
 RT "HIV-1 group O phylogenetic analysis of C2-gp41 region."



LT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RA EMBL: AJ135513, AB56216, J, 1.  
 RA EMBL: AF000000, AB56216, J, 1.  
 RA Interpro: IPR000777, GP20.  
 DR Pfam: PF00516, GP120, 1.  
 DR Pfam: PF00517, GP41, 1.  
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 FT NON\_TER 1 535  
 FT NON\_TER 1 535  
 SQ SEQUENCE 535 AA, 59662 MW, 7234583760DD12C5 CRC64;  
 Query Match 90.6%; Score 115; DB 15; Length 535;  
 Best Local Similarity 86.4%; Pred. No. 1.7e-09;  
 Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Db 374 L1SLMGCKRGLVCTYSVQNNET 22  
 374 L1SLMGCKRGLVCTYSVQNNET 395

LT 14  
 ID O91H08 PRELIMINARY; PRT; 125 AA.  
 AC O91H08  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (fragment).  
 GN GP41.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxId=11676;  
 RX MEDLINE=20386754; PubMed=10931623;  
 RC STRAIN=97CWT664;  
 RA Yang C., Gao F., Fonjongo P.N., Zekeng L., van der Groen G.,  
 RA Plenzazek D., Schable C., Lal R.B.,  
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
 RT type 1 group O.";  
 RL AIDS Res Hum Retroviruses 16:1075-1081 (2000).  
 RD EMBL: AJ135513, AB56216, J, 1.  
 DR Interpro: IPR000328, Env\_GP41.  
 DR Pfam: PF00517, GP41, 1.  
 KW Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 125 125  
 SQ SEQUENCE 125 AA, 15108 MW, EA296C4B25FP342 CRC64;  
 ary Match 89.8%; Score 114; DB 15; Length 125;  
 Best Local Similarity 77.3%; Pred. No. 6e-10;  
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 1 L1SLMGCKRGLVCTYSVQNNET 22  
 Db 37 L1SLMGCKRGLVCTYSVQNNET 58

RESULT 15  
 Q91EA9 PRELIMINARY; PRT; 230 AA.  
 ID Q91EA9  
 AC Q91EA9  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE GP41 (fragment).  
 GN Env.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxId=11676;  
 RX MEDLINE=20386754; PubMed=10931623;  
 RC STRAIN=97CWT664;  
 RA Yang C., Gao F., Fonjongo P.N., Zekeng L., van der Groen G.,  
 RA Plenzazek D., Schable C., Lal R.B.,  
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
 RT type 1 group O.";  
 RL AIDS Res Hum Retroviruses 16:1075-1081 (2000).  
 RD EMBL: AJ135513, AB56216, J, 1.  
 DR Interpro: IPR000328, Env\_GP41.  
 DR Pfam: PF00517, GP41, 1.  
 KW Transmembrane.  
 FT NON\_TER 1 230  
 FT NON\_TER 1 230  
 SQ SEQUENCE 230 AA, 28296 MW, 4B859829A69CCT43 CRC64;  
 Query Match 89.8%; Score 114; DB 15; Length 230;  
 Best Local Similarity 81.8%; Pred. No. 1.1e-09;  
 Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
 RA Philippe M., "Analysis and sub-typing of 47 HIV-1 group O isolates."  
 RA Phylogenetic Anal. and Sub-typing of HIV-1 Group O Isolates.  
 RA EMBL: AJ136411, AB56216, J, 1.  
 RA Interpro: IPR000328, Env\_GP41.  
 DR Pfam: PF00517, GP41, 1.  
 KW Transmembrane.  
 FT NON\_TER 1 230  
 FT NON\_TER 1 230  
 SQ SEQUENCE 230 AA, 28296 MW, 4B859829A69CCT43 CRC64;  
 Query Match 89.8%; Score 114; DB 15; Length 230;  
 Best Local Similarity 81.8%; Pred. No. 1.1e-09;  
 Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 Db 58 L1SLMGCKRGLVCTYSVQNNET 79

Search completed: May 29, 2003, 10:35:15  
 Job time : 23.6984 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:30:20 (Search time 29.333 Seconds  
(without alignments)  
99.938 Million cell updates/sec

Title: US-09-147-362a-3

Perfect score: 127

Sequence: 1 LLSMCKGRGLVCTSYQNMET 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

L number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: A: Geneseq 101002.\*

1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*

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23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	100.0	22	AA80461	Peptide derived from
2	122	96.5	22	AA80462	Peptide derived from
3	120	94.5	40	AA80463	Peptide derived from
4	118	92.9	22	AA80464	Peptide derived from
5	118	92.9	22	AA80465	Peptide derived from
6	117	92.1	32	AA80466	Peptide derived from
7	117	92.1	32	AA80467	Peptide derived from
8	113	89.0	22	AA80468	Peptide derived from
9	113	89.0	22	AA80469	Peptide derived from
10	113	89.0	40	AA80470	Peptide derived from

11	113	89.0	113	20	AAV05565	HIV-1 group O iso1
12	113	89.0	200	21	AAV77373	HIV-1 group O env
13	113	89.0	212	20	AAV06982	Recombinant pCO-8P
14	113	89.0	215	21	AAV77374	HIV-1 group O env
15	113	89.0	245	20	AAV09493	HIV-1 group O env
16	113	89.0	245	20	AAV06977	Recombinant pCO-9P
17	113	89.0	245	21	AAV77369	HIV-1 group O pCO-
18	113	89.0	281	21	AAV77367	HIV-1 group O env
19	113	89.0	333	20	AAV09507	HIV-1 group O env
20	113	89.0	372	20	AAV06975	HIV-1 group O env
21	113	89.0	460	20	AAV09500	Recombinant pCO-11
22	113	89.0	460	20	AAV06984	HIV-1 group O env
23	113	89.0	460	21	AAV77375	HIV-1 group O env
24	113	89.0	474	21	AAV77371	HIV-1 group O env
25	113	89.0	488	20	AAV09504	HIV-1 group O and
26	113	89.0	490	20	AAV06946	Recombinant pCO-9C
27	113	89.0	490	20	AAV77370	HIV-1 group O env
28	113	89.0	526	20	AAV09505	HIV-1 group O poly
29	113	89.0	618	20	AAV09496	HIV-1 group O env
30	113	89.0	618	20	AAV06980	Recombinant pCO-11
31	113	89.0	618	21	AAV77372	HIV-1 group O env
32	113	89.0	706	20	AAV09502	HIV-1 group O iso1
33	113	89.0	715	20	AAV09502	HIV-1 group O iso1
34	113	89.0	715	20	AAV09502	HIV-1 group O iso1
35	113	89.0	873	20	AAV09501	HIV-1 group O env
36	113	89.0	873	20	AAV06985	Amino acid sequenc
37	113	89.0	873	21	AAV77376	Peptide derived from
38	113	89.0	873	21	AAV77376	Peptide derived from
39	113	89.0	873	21	AAV77376	Peptide derived from
40	111	87.4	32	19	AA80470	Peptide derived from
41	111	87.4	33	21	AA81232	Peptide derived from
42	110	86.6	33	21	AA80449	Peptide derived from
43	110	86.6	33	21	AA81231	Peptide derived from
44	110	86.6	33	21	AA81231	Peptide derived from
45	110	86.6	40	17	AAW0343	Partial sequence O

## ALIGNMENTS

## RESULT 1

AA80461 standard; peptide; 22 AA.

AA80461:

28-DNR-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

W09845323-A1.

15-OCT-1998.

06-APR-1998. 98MO-FR00691.

24-FEB-1998. 98FR-000212.

09-APR-1997. 97FR-0001358.

(SNP) PASTEUR SANOPI DIAGNOSTICS SA.

Chenebaux DMB, Delageau JFH, Gabelle SJX, Rieunier FY;

WPI; 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by

human immune deficiency virus of group O

PS Claim 6; Page 42; 55pp; French.

XX  
CC AAM80459-74 represent synthetic peptides (either linear or cyclised by  
CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
CC connected around short highly conserved sequences present in isolates  
CC of group O human immune deficiency virus (HIV). The peptides are  
CC useful as immunological reagents for detecting infection by group O  
CC human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 100.0%; Score 127; DB 19; Length 22;

Best Local Similarity 100.0%; Pred. No. 6, 2e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 LLSMCKGRLVCTYSVQNMET 22  
DB 1 LLSMCKGRLVCTYSVQNMET 22

LT 2

AM80466 standard; peptide; 22 AA.

AAW80462;

28-JUN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

MO9845323-A1.

15-OCT-1998.

06-APR-1998; 98NO-FR00691.

24-FEB-1998; 98PR-0002212.

09-APR-1997; 97PR-0004356.

(SNP) PASTEUR SANOFI DIAGNOSTICS SA.

Cheneaux DMB, Delagreau JFH, Gabelle SIX, Rieunier FY;

WPI; 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by

human immune deficiency virus of group O

Claim 6; Page 43; 55pp; French.

AAM80459-74 represent synthetic peptides (either linear or cyclised by

Cys-Cys disulphide bonds). The peptides represent variable sequences

connected around short highly conserved sequences present in isolates

of group O human immune deficiency virus (HIV). The peptides are

useful as immunological reagents for detecting infection by group O

human immune deficiency virus (HIV).

Sequence 22 AA;

Query Match 97.6%; Score 124; DB 19; Length 22;

Best Local Similarity 95.5%; Pred. No. 1, 5e-09;  
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

AM80466 standard; peptide; 22 AA.

AAW80462;

28-JUN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

MO9845323-A1.

15-OCT-1998.

06-APR-1998; 98NO-FR00691.

24-FEB-1998; 98PR-0002212.

09-APR-1997; 97PR-0004356.

(SNP) PASTEUR SANOFI DIAGNOSTICS SA.

Cheneaux DMB, Delagreau JFH, Gabelle SIX, Rieunier FY;

WPI; 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by

human immune deficiency virus of group O

Claim 6; Page 42; 55pp; French.

AAM80459-74 represent synthetic peptides (either linear or cyclised by

Cys-Cys disulphide bonds). The peptides represent variable sequences

connected around short highly conserved sequences present in isolates

of group O human immune deficiency virus (HIV). The peptides are

useful as immunological reagents for detecting infection by group O

human immune deficiency virus (HIV).

Sequence 22 AA;

Query Match 96.1%; Score 123; DB 19; Length 22;

Best Local Similarity 95.5%; Pred. No. 2, 8e-07;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSMCKGRLVCTYSVQNMET 22  
DB 1 LLSMCKGRLVCTYSVQNMET 22

AM807346

AMW07346 standard; peptide; 40 AA.

AAW07346;

03-JUN-1997 (first entry)

Partial sequence of gp41 from HIV-1 gp. O strain BC97 (MAN).

Human immunodeficiency virus type 1, HIV-1; envelop; group M; group O;

C239-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;

immunogen; antibody.

Human immunodeficiency virus type 1.

[illegible]

XX	WPI, 1998-583190/49.			
XX	New synthetic peptide(s) - useful for, e.g. detecting infection by			
XX	human immune deficiency virus of group O			
PS	Claim 6; Page 42; 55pp; French.			
CC	AA060450-74 represent synthetic peptides (either linear or cyclised by			
CC	Cys-Cys disulphide bonds). The peptides represent variable sequences			
CC	connected around short highly conserved sequences adjacent to the			
CC	Cys-Cys disulphide bonds. The peptides are			
CC	useful as immunological reagents for detecting infection by group O			
CC	human immune deficiency virus (HIV).			
XX				
XX	Sequence 22 AA:			
XX				
XX	Query Match 92.9%; Score 118; DB 19; Length 22;			
XX	Best Local Similarity 90.9%; Freq. No. 9.3e-09;			
XX	Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
XX				
XX	1 LLSIMCKRGLVCTSVOMNET 22			
XX	1 LLSIMCKRGLVCTSVOMNET 22			
XX				
XX	RESULT 6			
XX	AA060463			
XX	AA060463 standard; peptide, 22 AA.			
XX				
XX	AA060463:			
XX				
XX	28-JAN-1999 (first entry)			
XX				
XX	Peptide derived from a conserved sequence of group O human HIV.			
XX				
XX	Group O human immune deficiency virus; HIV; detection; infection.			
XX				
XX	Synthetic.			
OS	OS Immune deficiency virus.			
XX				
XX	W09845323-A1.			
XX				
XX	15-OCT-1998.			
XX				
XX	06-APR-1998; 98MO-FR00691.			
XX				
XX	24-FEB-1998; 98FR-0002212.			
XX	09-APR-1997; 97FR-0004356.			
XX				
XX	(SNF1) PASTEUR SMOPT DIRMOSTICS SA.			
XX				
XX	Cheneboux DMB, Delagreau JFH, Gaddelle SXH, Rieunier PY;			
XX	WPI; 1998-583190/49.			
XX				
XX	New synthetic peptide(s) - useful for, e.g. detecting infection by			
XX	human immune deficiency virus of group O			
XX				
XX	Claim 6; Page 42; 55pp; French.			
XX				
XX	AA060459-74 represent synthetic peptides (either linear or cyclised by			
XX	Cys-Cys disulphide bonds). The peptides represent variable sequences			
XX	connected around short highly conserved sequences present in isolates			
XX	of group O human immune deficiency virus (HIV). The peptides are			
XX	useful as immunological reagents for detecting infection by group O			
XX	human immune deficiency virus (HIV).			
XX				
XX	Sequence 22 AA:			
XX				
XX	Query Match 92.9%; Score 118; DB 19; Length 22;			
XX	Best Local Similarity 90.9%; Freq. No. 9.3e-09;			
XX	Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
XX				
XX	1 LLSIMCKRGLVCTSVOMNET 22			
XX	1 LLSIMCKRGLVCTSVOMNET 22			
XX				
XX	RESULT 6			
XX	AA060463			
XX	AA060463 standard; peptide, 22 AA.			
XX				
XX	AA060463:			
XX				
XX	28-JAN-1999 (first entry)			
XX				
XX	Peptide derived from a conserved sequence of group O human HIV.			
XX				
XX	Group O human immune deficiency virus; HIV; detection; infection.			
XX				
XX	Synthetic.			
OS	OS Immune deficiency virus.			
XX				
XX	W09845323-A1.			
XX				
XX	15-OCT-1998.			
XX				
XX	06-APR-1998; 98MO-FR00691.			
XX				
XX	24-FEB-1998; 98FR-0002212.			
XX	09-APR-1997; 97FR-0004356.			
XX				
XX	(SNF1) PASTEUR SMOPT DIRMOSTICS SA.			
XX				
XX	Cheneboux DMB, Delagreau JFH, Gaddelle SXH, Rieunier PY;			
XX	WPI; 1998-583190/49.			
XX				
XX	New synthetic peptide(s) - useful for, e.g. detecting infection by			
XX	human immune deficiency virus of group O			
XX				
XX	Claim 6; Page 42; 55pp; French.			
XX				
XX	AA060459-74 represent synthetic peptides (either linear or cyclised by			
XX	Cys-Cys disulphide bonds). The peptides represent variable sequences			
XX	connected around short highly conserved sequences present in isolates			
XX	of group O human immune deficiency virus (HIV). The peptides are			
XX	useful as immunological reagents for detecting infection by group O			
XX	human immune deficiency virus (HIV).			
XX				
XX				

QY 1 LLSMCKGRALVCYTSVQNNET 22  
 DB 1 LLSMCKGRALVCYTSVQNNST 22

RESULT 7  
 AAM80469 standard; peptide: 32 AA.

AAM80469;  
 28-JAN-1999 (first entry)  
 Peptide derived from a conserved sequence of group O human HIV.  
 Group O human immune deficiency virus; HIV; detection; infection.  
 Synthetic.  
 Immune deficiency virus.

MO9845323-A1.  
 15-OCT-1998.  
 06-APR-1998; 98WO-FR00691.  
 24-FEB-1998; 98FR-0002212.  
 09-APR-1997; 97FR-0004356.  
 (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.  
 Chenebaux DMB, Delagneau JFH, Gabelle SIX, Rieunier FY;  
 WPI: 1998-583190/49.  
 New synthetic peptide(s) - useful for, e.g. detecting infection by  
 human immune deficiency virus of group O

Claim 6; Page 44; 55pp; French.

AAM80469-74 represent synthetic peptides (either linear or cyclised by  
 Cys-Cys disulphide bonds). The peptides represent variable sequences  
 connected around short highly conserved sequences present in isolates  
 of group O human immune deficiency virus (HIV). The peptides are  
 useful as immunological reagents for detecting infection by group O  
 human immune deficiency virus (HIV).

Sequence 32 AA:  
 Query Match 92.1%; Score 117; DB 19; Length 32;  
 Best Local Similarity 86.4%; Pred. NO. 1.8e-08;  
 Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSMCKGRALVCYTSVQNNET 22  
 DB 1 LLSMCKGRALVCYTSVQNNST 32

RESULT 8  
 AAM80464 standard; peptide: 22 AA.

AAM80464;  
 28-JAN-1999 (first entry)  
 Peptide derived from a conserved sequence of group O human HIV.  
 Group O human immune deficiency virus; HIV; detection; infection.  
 Synthetic.  
 Immune deficiency virus.

XX MO9845323-A1.  
 XX 15-OCT-1998.  
 XX 06-APR-1998; 98WO-FR00691.  
 XX 24-FEB-1998; 98FR-0002212.  
 XX 09-APR-1997; 97FR-0004356.  
 XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.  
 XX Chenebaux DMB, Delagneau JFH, Gabelle SIX, Rieunier FY;  
 XX WPI: 1998-583190/49.  
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by  
 XX human immune deficiency virus of group O  
 XX Claim 6; Page 43; 55pp; French.

XX AAM80459-74 represent synthetic peptides (either linear or cyclised by  
 XX Cys-Cys disulphide bonds). The peptides represent variable sequences  
 XX connected around short highly conserved sequences present in isolates  
 XX of group O human immune deficiency virus (HIV). The peptides are  
 XX useful as immunological reagents for detecting infection by group O  
 XX human immune deficiency virus (HIV).

XX Sequence 22 AA:  
 Query Match 89.0%; Score 113; DB 19; Length 22;  
 Best Local Similarity 81.8%; Pred. NO. 4.1e-06;  
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSMCKGRALVCYTSVQNNET 22  
 DB 1 LLSMCKGRALVCYTSVQNNST 22

RESULT 9  
 AAM80465 standard; peptide: 22 AA.

AAM80465;  
 28-JAN-1999 (first entry)  
 Peptide derived from a conserved sequence of group O human HIV.  
 Group O human immune deficiency virus; HIV; detection; infection.  
 Synthetic.  
 Immune deficiency virus.

MO9845323-A1.  
 15-OCT-1998.  
 06-APR-1998; 98WO-FR00691.  
 24-FEB-1998; 98FR-0002212.  
 09-APR-1997; 97FR-0004356.  
 (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.  
 Chenebaux DMB, Delagneau JFH, Gabelle SIX, Rieunier FY;  
 WPI: 1998-583190/49.  
 New synthetic peptide(s) - useful for, e.g. detecting infection by  
 human immune deficiency virus of group O  
 Claim 6; Page 43; 55pp; French.

XX AA0459-74 represent synthetic peptides (either linear or cyclized by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 CC  
 XX Sequence 22 AA:  
 SO  
 Query Match 89.0%; Score 113; DB 19; Length 22;  
 Best Local Similarity 86.4%; Pctid No 4.1e-08;  
 Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 LLSMCKGRGLVCTYSVQNMET 22  
 Db 1 LLSMCKGRGLVCTYSVQNMET 22  
 XX  
 XX RESULT 10  
 XX AA07352 standard; peptide: 40 AA.  
 XX  
 XX AA07352:  
 XX  
 XX 03-JUN-1997 (first entry)  
 XX  
 XX Partial sequence of gp41 from HIV-1 gp. O strain BCP13.  
 XX  
 XX Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;  
 XX C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;  
 XX primer; hybridisation; amplification; PCR; polymerase chain reaction;  
 XX immunogen; antibody.  
 XX  
 XX Human immunodeficiency virus type 1.  
 XX  
 XX W0567013-A1.  
 XX  
 XX 06-SEP-1996.  
 XX  
 XX 26-FEB-1996; 96MO-FR00294.  
 XX  
 XX 27-FEB-1995; 95FR-0002236.  
 XX  
 XX (ASST-) ASSISTANCE PUBLIQUE HOPITALUX PARIS.  
 XX (INRM-) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX  
 XX Chaix-Baudier ML, Lousselet-Ajaka I, Ly T, Saragosti S, Simon F,  
 XX WPI; 1996-41279/41.  
 XX  
 XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
 XX antibodies - useful for diagnosis, screening and typing, or as  
 XX immunogens  
 XX  
 XX Claim 12; Page 46; 71pp; French.  
 XX  
 XX Human immunodeficiency virus type 1 (HIV-1) strains are currently  
 XX divided into 2 major groups based on the nucleotide sequences of the  
 XX envelope gene (env): group M containing sub-groups A-G, and group O  
 XX containing the strains AM70 and WY8190. The invention relates to the  
 XX discovery of several new strains of HIV-1 which can be placed in group O,  
 XX based on the partial sequences of the C2V3-env, gp41 and gag genes (see  
 XX AA045907-39 and AA070129-64). The novel strains have been deposited as  
 XX (MN1), 1547 (BCF08 (MKO)) and 145 (BCF03 (POC)). The sequence  
 XX (MN1), 1547 (BCF08 (MKO)) and 145 (BCF03 (POC)). The sequence  
 XX presented here is from the strain BCP13 and corresponds to a fragment of  
 XX the gp41 protein encoded by the env gene. The nucleic acids can be used  
 XX to detect gp. O HIV-1 strains by hybridisation or (as primers) by gene  
 XX amplification, also for screening and typing of such strains. Peptides  
 XX encoded by the nucleic acids can be used as immunogens to raise Ab for  
 XX detecting gp. O HIV-1.

SO Sequence 40 AA:  
 Query Match 89.0%; Score 113; DB 17; Length 40;  
 Best Local Similarity 82.4%; Pctid No 7.1e-09;  
 Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 LLSMCKGRGLVCTYSVQNMET 22  
 Db 19 LLSMCKGRGLVCTYSVQNMET 40  
 XX  
 XX RESULT 11  
 XX AA05565 standard; Protein; 113 AA.  
 XX  
 XX AA05565:  
 XX  
 XX 19-JUL-1999 (first entry)  
 XX  
 XX HIV-1 group O isolate MP539-PBMC gp41 antigen.  
 XX  
 XX HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;  
 XX vaccine; diagnosis; AIDS.  
 XX  
 XX Human immunodeficiency virus type 1.  
 XX  
 XX Key location/qualifiers  
 XX  
 XX Misc-difference 65 /note= "encoded by MMW"  
 XX  
 XX Misc-difference 74 /note= "encoded by ATP"  
 XX  
 XX Misc-difference 84 /note= "encoded by GAK"  
 XX  
 XX Misc-difference 9 /note= "encoded by AGV"  
 XX  
 XX W03904011-A2.  
 XX  
 XX 28-JAN-1999.  
 XX  
 XX 20-JUL-1996; 96MO-EP04522.  
 XX  
 XX 18-JUL-1997; 97EP-0870110.  
 XX  
 XX (INNO-) INNOGENETICS NV.  
 XX  
 XX Delaporte E, Feeters M, Saman E, Vanden Haesevelde M;  
 XX WPI; 1999-113255/11.  
 XX N-PSDB; AA05565.  
 XX  
 XX New isolated HIV-1 group O strains - used to produce  
 XX polynucleotides, antigens and antibodies for use in diagnosis and in  
 XX vaccines for prevention of HIV-1 infection  
 XX  
 XX Claim 3; Fig 6; 162pp; English.  
 XX  
 XX The present sequence is an antigen of the gp41 protein of HIV-1  
 XX group O (Outlier) strain MP539-PBMC, a Cameroon isolate. The  
 XX invention relates to new HIV-1 group O antigens (see AA05546-625),  
 XX and the use of these antigens, or nucleic acids encoding them (see  
 XX AA03154-80), in the diagnosis and prophylaxis of AIDS. They can be  
 XX used as reagents for detecting HIV-1 group O infection and for  
 XX differentiating different types of immunity against HIV-1 infection, in  
 XX particular against HIV-1 group O infection, "compares at least one"  
 XX HIV-1 type O antigen, a nucleic acid encoding such an antigen, a  
 XX virus-like particle comprising such an antigen, or an attenuated  
 XX form of an HIV-1 type O strain. The invention also relates to new  
 XX HIV-1 group O strains, mostly from patients from Cameroon and its  
 XX neighbouring countries.  
 XX  
 XX Sequence 113 AA.







CC antigens from HIV-group M and HIV-2 antigens. Sequences AY77369-v77375  
represent recombinant HIV-1 group O env antigens encoded by the synthetic  
genes AZ90280-290286. The recombinant HIV-1 env proteins contain  
various deletions relative to the native HAM112 isolate env protein  
1(AAY77376). The recombinant HIV-1 group O antigens were purified and used  
to screen hybridoma cultures.  
XX  
SQ Sequence 215 AA;  
Query Match 89.0%; Score 113; DB 21; Length 215;  
Best Local Similarity 81.8%; Pred.No. 3.5e-07;  
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
OY 1 LLSWCKGRIHVCYTSVNNET 22  
||:|||||:|||||  
DB 127 LLLWCKGRIHVCYTSVNNET 148  
||:|||||:|||||

Search completed: May 29, 2003, 10:36:21  
Time : 30.333 sec

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:36, Search time 9.95238 Seconds

(without alignments) 65,040 Million cell updates/sec

Title: US-09-147-362a-3

Sequence: 1 LUSMCKGRVICYTSQVNNRT 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgm2\_6/p/cdata/1/aa/6B.COMB.pap.\*

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20: /cgm2\_6/p/cdata/1/aa/14B.COMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	120	94.5	40	3	US-08-894-699-39
2	120	94.5	40	3	US-09-444-410-19
3	113	89.0	40	4	US-08-894-699-48
4	113	89.0	40	4	US-08-894-699-48
5	113	89.0	40	4	US-08-894-699-48
6	113	89.0	40	4	US-08-894-699-48
7	113	89.0	40	4	US-08-894-699-48
8	113	89.0	40	4	US-08-894-699-48
9	113	89.0	40	4	US-08-894-699-48
10	113	89.0	40	4	US-08-894-699-48
11	113	89.0	40	4	US-08-894-699-48
12	113	89.0	40	4	US-08-894-699-48
13	113	89.0	40	4	US-08-894-699-48
14	113	89.0	40	4	US-08-894-699-48
15	113	89.0	40	4	US-08-894-699-48
16	113	89.0	40	4	US-08-894-699-48
17	113	89.0	40	4	US-08-894-699-48
18	113	89.0	40	4	US-08-894-699-48
19	113	89.0	40	4	US-08-894-699-48
20	113	89.0	40	4	US-08-894-699-48
21	113	89.0	40	4	US-08-894-699-48
22	113	89.0	40	4	US-08-894-699-48
23	113	89.0	40	4	US-08-894-699-48
24	113	89.0	40	4	US-08-894-699-48
25	113	89.0	40	4	US-08-894-699-48
26	113	89.0	40	4	US-08-894-699-48
27	113	89.0	40	4	US-08-894-699-48

28	107	84.3	40	4	US-09-444-410-41	Sequence 41, Appl
29	107	84.3	40	4	US-09-444-410-41	Sequence 42, Appl
30	107	84.3	40	4	US-09-444-410-41	Sequence 43, Appl
31	106	83.5	40	3	US-08-894-699-37	Sequence 37, Appl
32	106	83.5	40	4	US-09-444-410-37	Sequence 37, Appl
33	106	83.5	104	4	US-08-817-441-100	Sequence 100, Appl
34	105	82.7	40	3	US-08-894-699-40	Sequence 40, Appl
35	105	82.7	40	3	US-09-444-410-40	Sequence 40, Appl
36	104	81.9	23	4	US-09-444-410-40	Sequence 40, Appl
37	104	81.9	23	4	US-09-444-410-40	Sequence 40, Appl
38	104	81.9	23	4	US-09-444-410-40	Sequence 40, Appl
39	104	81.9	23	4	US-09-444-410-40	Sequence 40, Appl
40	104	81.9	23	4	US-09-444-410-40	Sequence 40, Appl
41	104	81.9	42	3	US-08-894-699-66	Sequence 66, Appl
42	104	81.9	42	4	US-09-444-410-66	Sequence 66, Appl
43	103	81.1	33	4	US-09-444-410-66	Sequence 66, Appl
44	103	81.1	33	4	US-09-444-410-66	Sequence 66, Appl
45	103	81.1	33	4	US-09-444-410-66	Sequence 66, Appl

## ALIGNMENTS

RESULT 1  
US-08-894-699-39  
Sequence 39, Appl  
Patent No. 6,010,769  
GENERAL INFORMATION:  
APPLICANT: SARACOSTI, SIMON, FRANCOIS  
APPLICANT: LOUISBERT-AJARA, IBITISSM  
APPLICANT: LY, THON-DUONG  
APPLICANT: LAM, HAN-BAO, LAURE  
TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,  
STREET: 1755 SOUTH DEPPERSON DAVIS HIGHWAY, FOURTH  
FLOOR, ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
PRIOR APPLICATION DATA: 1996  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-2220  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
FUNCTIONS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-08-894-699-39

Query Match 94.5%; Score 120; DB 3; Length 40;  
Best Local Similarity 90.9%; Pred. No. 9.3e-11;  
Matches 20; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 LLSNMGCKGRIVCTSYVMNET 22  
19 LLSNMGCKGRIVCTSYVMNET 40

RESULT 2  
US-09-444-410-39

Sequence 39, Application US/09444410  
Patent No. 6270975

GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOS  
APPLICANT: LOUSBERT-AJARA, IBITTSSAM  
APPLICANT: LY THOI-DUONG, MARIE-LAURE  
TITLE OF INVENTION: GROUP C HIV-1, FRAGMENTS OF SUCH  
TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESS: P.O. BOX, SPVAK, MCCLELLAND, MAIER & NEUSTADT,  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/894,699  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 26-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-OPCT  
TELEPHONE: 703-413-3100  
FAX: 703-413-3100  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-444-410-39

Query Match 94.5%; Score 120; DB 3; Length 40;  
Best Local Similarity 90.9%; Pred. No. 9.3e-11;  
Matches 20; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 LLSNMGCKGRIVCTSYVMNET 22  
19 LLSNMGCKGRIVCTSYVMNET 40

RESULT 3  
US-08-894-699-68

Sequence 68, Application US/08894699  
Patent No. 6030769

GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOS  
APPLICANT: LOUSBERT-AJARA, IBITTSSAM  
APPLICANT: LY THOI-DUONG, MARIE-LAURE  
TITLE OF INVENTION: GROUP C HIV-1, FRAGMENTS OF SUCH  
TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESS: P.O. BOX, SPVAK, MCCLELLAND, MAIER & NEUSTADT,  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 26-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-OPCT  
TELEPHONE: 703-413-3100  
FAX: 703-413-3100  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-68

Query Match 89.0%; Score 113; DB 3; Length 40;  
Best Local Similarity 86.4%; Pred. No. 9.4e-10;  
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LLSNMGCKGRIVCTSYVMNET 22  
19 LLSNMGCKGRIVCTSYVMNET 40

RESULT 4  
US-09-444-410-68

Sequence 68, Application US/09444410  
Patent No. 6270975

GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOS  
APPLICANT: LOUSBERT-AJARA, IBITTSSAM  
APPLICANT: LY THOI-DUONG, MARIE-LAURE  
TITLE OF INVENTION: GROUP C HIV-1, FRAGMENTS OF SUCH  
TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESS: P.O. BOX, SPVAK, MCCLELLAND, MAIER & NEUSTADT,  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 26-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-OPCT  
TELEPHONE: 703-413-3100  
FAX: 703-413-3100  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-444-410-68

TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USBS THEREOF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS: 81  
 ADDRESS: DEAN, STEVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ADDRESS: P.C.  
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 STREET: FLOOR  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22204  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/444,410  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/834,699  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PR 95/02236  
 FILING DATE: 2 FEB 1995  
 NAME: OELON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-3220  
 INFORMATION FOR SEQ ID NO: 68:  
 SEQUENCE CHARACTERISTICS: 68:  
 LENGTH: 40 amino acids  
 TYPE: amino acid  
 STANDARDS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-444-410-68

Query Match 89.0%; Score 113; DB 4; Length 40;  
 Best Local Similarity 86.4%; Pred. NO. 9.4e-10;  
 Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LLSMCKGRILCVTSYKNNET 22  
 19 LLSMCKGRILCVTSYKNNET 40

RESULT 5  
 US-08-912-129A-58  
 Sequence 58, Application US/08912129A  
 Patent No. 5925533  
 GENERAL INFORMATION:  
 APPLICANT: VALIARI, ANADRUZELA S.  
 APPLICANT: HACKETT, JOHN JR.  
 APPLICANT: HICOMAN, ROBERT K.  
 APPLICANT: VARITER, VINCENT A. JR.  
 APPLICANT: NECKLAMS, ELIZABETH A.  
 APPLICANT: GOLDEN, ALAN W.  
 APPLICANT: BRENNAN, CATHERINE A.  
 APPLICANT: SUSHIL, G.  
 TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION  
 NUMBER OF SEQUENCES: 89  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Abbott Laboratories  
 STREET: 100 Abbott Park Road  
 CITY: Abbott Park  
 STATE: IL  
 COUNTRY: USA

ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: MS-DOS (Windows 95)  
 SOFTWARE: Microsoft word (ASCII format output)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/912,129A  
 FILING DATE: 15-AUG-1997  
 CLASSIFICATION: 16  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Danckere, Andreas M.  
 REGISTRATION NUMBER: 32,652  
 REFERENCE/DOCKET NUMBER: 6109, US-01  
 TELEPHONE: 847-937-9803  
 TELEFAX: 847-938-2623

INFORMATION FOR SEQ ID NO: 58:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 215 amino acids  
 TYPE: amino acid  
 STANDARDS: single  
 TOPOLOGY: linear  
 US-08-912-129A-58

Query Match 89.0%; Score 113; DB 2; Length 215;  
 Best Local Similarity 81.8%; Pred. NO. 5.3e-09;  
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 LLSMCKGRILCVTSYKNNET 22  
 127 LLSMCKGRILCVTSYKNNET 148

RESULT 6  
 US-08-912-129A-48  
 Sequence 48, Application US/08912129A  
 Patent No. 5925533  
 GENERAL INFORMATION:  
 APPLICANT: VALIARI, ANADRUZELA S.  
 APPLICANT: HACKETT, JOHN JR.  
 APPLICANT: HICOMAN, ROBERT K.  
 APPLICANT: VARITER, VINCENT A. JR.  
 APPLICANT: NECKLAMS, ELIZABETH A.  
 APPLICANT: GOLDEN, ALAN W.  
 APPLICANT: BRENNAN, CATHERINE A.  
 APPLICANT: SUSHIL, G.  
 TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION  
 NUMBER OF SEQUENCES: 89  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Abbott Laboratories  
 STREET: 100 Abbott Park Road  
 CITY: Abbott Park  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
 OPERATING SYSTEM: MS-DOS (Windows 95)  
 SOFTWARE: Microsoft word (ASCII format output)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/912,129A  
 FILING DATE: 15-AUG-1997  
 CLASSIFICATION: 16  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:

NAME: Danckers, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109 US 01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX: 847-938-2623  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 245 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-912-129A-48

Query Match 89.0%; Score 113; DB 2; Length 245;  
Best Local Similarity 81.8%; Pred. No. 6e-09;  
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
1 LLSWGCKGRVLCYTSVMNET 22  
127 LNLWCKGRLLCYTSVMNET 148

Db 127 LNLWCKGRLLCYTSVMNET 148

RESULT 7  
US-08-912-129A-52  
Sequence 52; Application US/08912129A  
Patent No 5922513  
GENERAL INFORMATION:  
APPLICANT: VALLEARI, ANDRUZELA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: HICOMAN, ROBERT K.  
APPLICANT: VARITEK, VINCENT A. JR.  
APPLICANT: NECKLAW, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN M.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEVARE, SUSHIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
OPERATING SYSTEM: IBM Compatible  
SOFTWARE: Microsoft Word (ASCII format output)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,129A  
CLASS DATE: 15-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckers, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109 US 01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 245 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: Protein  
US-08-912-129A-52

Query Match 89.0%; Score 113; DB 2; Length 373;  
Best Local Similarity 81.8%; Pred. No. 9.3e-09;  
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
1 LLSWGCKGRVLCYTSVMNET 22  
127 LNLWCKGRLLCYTSVMNET 148

Db 127 LNLWCKGRLLCYTSVMNET 148

RESULT 8  
US-08-912-129A-60  
Sequence 60; Application US/08912129A  
Patent No 5922513  
GENERAL INFORMATION:  
APPLICANT: VALLEARI, ANDRUZELA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: HICOMAN, ROBERT K.  
APPLICANT: VARITEK, VINCENT A. JR.  
APPLICANT: NECKLAW, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN M.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEVARE, SUSHIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
OPERATING SYSTEM: IBM Compatible  
SOFTWARE: Microsoft Word (ASCII format output)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,129A  
CLASS DATE: 15-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckers, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109 US 01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 460 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-912-129A-60

Query Match 89.0%; Score 113; DB 2; Length 460;  
Best Local Similarity 81.8%; Pred. No. 1.2e-08;  
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
1 LLSWGCKGRVLCYTSVMNET 22  
372 LNLWCKGRLLCYTSVMNET 393

Db 372 LNLWCKGRLLCYTSVMNET 393

RESULT 9



```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,129A
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATORNEY/AGENT INFORMATION:
; NAME: Robert J. De Leys, Robert J.
; REGISTRATION NUMBER: 6109 US .01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-9803
; TELEFAX: 847-938-2623
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 873 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-912-129A-61
Query Match 89.0%; Score 113; DB 2; Length 873;
Best Local Similarity 81.8%; Pred. No. 2,2e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Cy 1 LLSWGCKGRIVCYTSVQNN 22
Db 601 LLSWGCKGRIVCYTSVQNN 622

RESULT 12
US-09-433-428D-6
; Sequence 6, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; STRANDEDNESS: single
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: PPT
; ORIGIN: Human immunodeficiency virus type 1
; US-09-433-428D-6
Query Match 87.4%; Score 111; DB 4; Length 33;
Best Local Similarity 90.0%; Pred. No. 1,5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LLSWGCKGRIVCYTSVQNN 20
Db 14 LLSWGCKGRIVCYTSVQNN 33

RESULT 13
US-09-433-428D-25
; Sequence 25, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 33
; TYPE: PPT
; ORIGIN: Human immunodeficiency virus type 1
; US-09-433-428D-25
Query Match 86.6%; Score 110; DB 4; Length 33;
Best Local Similarity 90.0%; Pred. No. 2,1e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LLSWGCKGRIVCYTSVQNN 20
Db 14 LLSWGCKGRIVCYTSVQNN 33

RESULT 14
US-08-894-699-36
; Sequence 36, Application US/08894699
; Patent No. 6030769
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANKIS
; APPLICANT: LONSFEST, ARAB
; APPLICANT: LY, THOI-DUONG, MARIE-LAURE
; APPLICANT: CHAIK-BANDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; NUMBER OF SEQUENCES: 81
; COMPLETION ADDRESS: 81
; ADDRESS: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; ADDRESS: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: 108/894,699
; FILING DATE: 1997-05-28
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/00294
; FILING DATE: 26-FEB-1996
; APPLICATION NUMBER: FR 95/02236
; PUBLICATION NUMBER: 1995
; ATORNEY/AGENT INFORMATION:
; NAME: OBLON, NORWAY F.
; REGISTRATION NUMBER: 24,614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-3000
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-894-699-36
Query Match 86.6%; Score 110; DB 3; Length 40;
Best Local Similarity 81.8%; Pred. No. 2,5e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```



Thu May 29 15:12:5:09 2003

QY 1 LLSWGCKGRIVCTYSVQNNET 22  
 ||:|||||:|||||:|||||  
 Db 19 LLSWGCKGRIVCTYSVQNNMT 40

## RESULT 15

US-09-444-410-36  
 ; Sequence 36, Application US/09444410  
 ; Patent No. 6270975

## GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS  
 APPLICANT: SARREST, GUYOBE  
 APPLICANT: LUSSEST, JANA IBTISSEM  
 APPLICANT: LY THOAI-DHONG  
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 NUMBER OF SEQUENCES: 81

## CORRESPONDENCE ADDRESS:

ADDRESSEE: GILSON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ADDRESS: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 STREET, FLOOR  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA

## COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
 MEDIUM TYPE: floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA: US/09/444,410

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/894,699

## FILING DATE:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236

## FILING DATE:

27-FEB-1995

## REGISTRATION NUMBER:

24,614

## REFERENCE/DOCKET NUMBER:

0354-0020-0PCT

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

## TELEFAX:

703-413-2220

## INFORMATION FOR SEQUENCING:

36:

## SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids

## TYPE:

amino acid

## STRANDEDNESS:

single

## TOPOLOGY:

linear

## MOLECULE TYPE:

peptide

## US-09-444-410-36

Query Match 86.6%; Score 110; DB 4; Length 40;  
 Best Local Similarity 81.8%; Pred. No. 2.5e-09;  
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCTYSVQNNET 22  
 ||:|||||:|||||:|||||  
 Db 19 LLSWGCKGRIVCTYSVQNNMT 40

Search completed: May 29, 2003, 10:41:27  
 Job time : 9.95238 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1995 - 2003 CompuGen Ltd.

OM protein - protein search, using ew model

Run on: May 29, 2003, 10:39:21 : Search time 19.0317 Seconds

(without alignments)  
117.011 Million cell updates/sec

Title: US-09-147-362A-3

Sequence: 1 LLSWGGKGRRLVCTSYVMNWT 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223594 residues

1 number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB pep:\*

2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB pep:\*

3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB pep:\*

4: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB pep:\*

5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB pep:\*

6: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB pep:\*

7: /cgn2\_6/prodata/2/pubpaa/PCTUS\_PUBCOMB pep:\*

8: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB pep:\*

9: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB pep:\*

10: /cgn2\_6/prodata/2/pubpaa/US09\_PUBCOMB pep:\*

11: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB pep:\*

12: /cgn2\_6/prodata/2/pubpaa/US10\_PUBCOMB pep:\*

13: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB pep:\*

14: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113	89.0	215	1	US-08-911-824-58
2	113	89.0	245	1	US-08-911-824-58
3	113	89.0	245	1	US-08-911-824-58
4	113	89.0	273	1	US-08-911-824-52
5	113	89.0	460	1	US-08-911-824-60
6	113	89.0	488	1	US-08-911-824-65
7	113	89.0	490	1	US-08-911-824-50
8	113	89.0	526	1	US-08-911-824-97
9	113	89.0	618	1	US-08-911-824-54
10	113	89.0	716	1	US-08-911-824-53
11	113	89.0	716	1	US-08-911-824-53
12	113	89.0	873	1	US-08-911-824-61
13	109	85.8	37	9	US-10-026-741-86
14	109	85.8	200	10	US-09-854-816-104
15	106	83.5	37	9	US-10-026-741-94
16	106	83.5	104	9	US-10-026-741-100
17	103	81.1	35	9	US-10-026-741-10
18	103	81.1	35	9	US-10-026-741-7
19	103	81.1	37	9	US-10-026-741-90

20	103	81.1	351	9	US-10-026-741-47	Sequence 47, Appl
21	103	81.1	87	9	US-10-026-741-102	Sequence 102, Appl
22	103	81.1	27	9	US-10-026-741-30	Sequence 30, Appl
23	101	79.5	37	9	US-10-026-741-88	Sequence 88, Appl
24	99	78.0	213	10	US-09-854-816-103	Sequence 103, App
25	96	75.6	23	9	US-09-388-847-4	Sequence 2, Appl1
26	96	75.6	23	9	US-10-000-321-2	Sequence 2, Appl1
27	96	75.6	24	9	US-10-026-741-34	Sequence 34, Appl
28	96	75.6	35	9	US-09-886-156-62	Sequence 62, Appl
29	96	75.6	35	9	US-09-886-156-62	Sequence 62, Appl
30	96	75.6	35	9	US-09-886-156-62	Sequence 62, Appl
31	96	75.6	35	9	US-09-886-156-62	Sequence 62, Appl
32	96	75.6	146	12	US-10-000-321-10	Sequence 10, Appl
33	96	75.6	204	10	US-09-854-816-105	Sequence 105, Appl
34	96	75.6	351	9	US-09-886-156-46	Sequence 46, Appl
35	96	75.6	351	9	US-09-886-156-46	Sequence 46, Appl
36	96	75.6	351	9	US-09-886-156-46	Sequence 46, Appl
37	96	75.6	351	9	US-09-886-156-46	Sequence 46, Appl
38	86	67.7	268	10	US-09-854-816-39	Sequence 39, Appl
39	84	66.1	37	9	US-10-026-741-84	Sequence 84, Appl
40	84	66.1	204	10	US-09-854-816-106	Sequence 106, Appl
41	82	64.6	198	10	US-09-854-816-81	Sequence 81, Appl
42	81	63.8	37	9	US-10-026-741-82	Sequence 82, Appl
43	81	63.8	198	10	US-09-854-816-70	Sequence 70, Appl
44	81	63.8	198	10	US-09-854-816-70	Sequence 70, Appl
45	81	63.8	198	10	US-09-854-816-60	Sequence 60, Appl

## ALIGNMENTS

RESULT 1

US-08-911-824-58

Sequence 58, Application US/08911824

Publication No. US20030004323A1

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Hackett, John R., Jr.

APPLICANT: Yamaguchi, Julie

APPLICANT: Bolden, Catherine A.

APPLICANT: Hitchman, Robert K.

APPLICANT: Devare, Shashi G.

TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV

FILE REFERENCE: 6165 US 01

CURRENT APPLICATION NUMBER: US/08/911,824

NUMBER OF SEQ ID NOS: 121-08-15

SOFTWARE: FASTED for Windows Version 3.0

SEQ ID NO 58

LENGTH: 215

TYPE: PRT

ORGANISM: Human Immunodeficiency Virus

FEATURES/KEY INFORMATION: Encodes recombinant protein pCO-8PL

US-08-911-824-58

Best Local Match

Query Match 89.0%, Score 113, DB 1, Length 215;

Query Similarity 81.8%, Pred. No. 7.7e+09;

Matches 18, Consecutive 3, Mismatches 1, Indels 0, Gaps 0;

1 LLSWGGKGRRLVCTSYVMNWT 22

DB 127 LLSWGGKGRRLVCTSYVMNWT 148

RESULT 2

US-08-911-824-48

Sequence 48, Application US/08911824

Publication No. US20030004323A1

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Hackett, John R., Jr.  
APPLICANT: Yamaguchi, Julie  
APPLICANT: Golden, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Devere, Shelli G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165 US 01  
CURRENT APPLICATION NUMBER: US/08/911,824  
CURRENT FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEO ID NO 52  
LENGTH: 245  
TYPE: PRF  
ORGANISM: Human Immunodeficiency Virus  
OTHER INFORMATION: Encodes recombinant protein pCO-9PL  
US-09-11-824-48  
Query Match 89.0%; Score 113; DB 1; Length 245;  
Best Local Similarity 81.8%; Pred. No. 6.7e-09;  
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRILCYTSVQWNET 22  
DB 127 LNLIMGCKGRILCYTSVQWNET 148

RESULT 3  
US-08-911-824-120  
Sequence 120; Application US/08911824  
Publication No. US20030004323A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Yamaguchi, Julie  
APPLICANT: Golden, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Devere, Shelli G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165 US 01  
CURRENT APPLICATION NUMBER: US/08/911,824  
CURRENT FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEO ID NO 120  
LENGTH: 281  
TYPE: PRF  
ORGANISM: Human Immunodeficiency Virus  
OTHER INFORMATION: Encodes recombinant protein pCO-15PL  
US-08-911-824-120

Query Match 89.0%; Score 113; DB 1; Length 281;  
Best Local Similarity 81.8%; Pred. No. 9.9e-09;  
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
OY 1 LLSWGCKGRILCYTSVQWNET 22  
DB 127 LNLIMGCKGRILCYTSVQWNET 148

RESULT 4  
US-08-911-824-52  
Sequence 52; Application US/08911824  
Publication No. US20030004323A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.

APPLICANT: Yamaguchi, Julie  
APPLICANT: Golden, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Devere, Shelli G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165 US 01  
CURRENT APPLICATION NUMBER: US/08/911,824  
CURRENT FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEO ID NO 52  
LENGTH: 373  
TYPE: PRF  
ORGANISM: Human Immunodeficiency Virus  
OTHER INFORMATION: Encodes recombinant protein pCO-11PL  
US-08-911-824-52

Query Match 89.0%; Score 113; DB 1; Length 373;  
Best Local Similarity 81.8%; Pred. No. 1.3e-08;  
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
OY 1 LLSWGCKGRILCYTSVQWNET 22  
DB 127 LNLIMGCKGRILCYTSVQWNET 148

RESULT 5  
US-08-911-824-60  
Sequence 60; Application US/08911824  
Publication No. US20030004323A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Yamaguchi, Julie  
APPLICANT: Golden, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Devere, Shelli G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165 US 01  
CURRENT APPLICATION NUMBER: US/08/911,824  
CURRENT FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEO ID NO 60  
LENGTH: 460  
TYPE: PRF  
ORGANISM: Human Immunodeficiency Virus  
OTHER INFORMATION: Encodes recombinant protein pCO-8CKS  
US-08-911-824-60

Query Match 89.0%; Score 113; DB 1; Length 460;  
Best Local Similarity 81.8%; Pred. No. 1.6e-08;  
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
OY 1 LLSWGCKGRILCYTSVQWNET 22  
DB 372 LNLIMGCKGRILCYTSVQWNET 193

RESULT 6  
US-08-911-824-96  
Sequence 95; Application US/08911824  
Publication No. US20030004323A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Yamaguchi, Julie

```

APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165.US.O1
CURRENT APPLICATION NUMBER: US/08/911.824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 95
LENGTH: 488
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-14PL
US-08-911-824-95

```

```

Query Match      89.0%; Score 113; DB 1; Length 488;
Best Local Similarity 81.8%; Pred. No. 1.7e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Oy 1 L15SMGCGKRLVCYTSYKNNET 22
Db 127 L14LMGCKGRILICTYSYKNNET 146

```

```

RESULT 7
US-08-911-824-50
Sequence 50, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamauchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165.US.O1
CURRENT APPLICATION NUMBER: US/08/911.824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 49
LENGTH: 480
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-9CKS
US-08-911-824-50

```

```

Query Match      89.0%; Score 113; DB 1; Length 490;
Best Local Similarity 81.8%; Pred. No. 1.7e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Oy 1 L15SMGCGKRLVCYTSYKNNET 22
Db 372 L14LMGCKGRILICTYSYKNNET 393

```

```

RESULT 8
US-08-911-824-97
Sequence 97, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamauchi, Julie
APPLICANT: Golden, Alan M.

```

```

APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165.US.O1
CURRENT APPLICATION NUMBER: US/08/911.824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 97
LENGTH: 526
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-15CKS
US-08-911-824-97

```

```

Query Match      89.0%; Score 113; DB 1; Length 526;
Best Local Similarity 81.8%; Pred. No. 1.8e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Oy 1 L15SMGCGKRLVCYTSYKNNET 22
Db 372 L14LMGCKGRILICTYSYKNNET 393

```

```

RESULT 9
US-08-911-824-54
Sequence 54, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamauchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165.US.O1
CURRENT APPLICATION NUMBER: US/08/911.824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 54
LENGTH: 618
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-11CKS
US-08-911-824-54

```

```

Query Match      89.0%; Score 113; DB 1; Length 618;
Best Local Similarity 81.8%; Pred. No. 2.1e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Oy 1 L15SMGCGKRLVCYTSYKNNET 22
Db 372 L14LMGCKGRILICTYSYKNNET 393

```

```

RESULT 10
US-08-911-824-93
Sequence 93, Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamauchi, Julie
APPLICANT: Golden, Alan M.

```

```

APPLICANT: Hickman, Robert K.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165.US.01
CURRENT APPLICATION NUMBER: US/08/911,824
NUMBER OF SEQ IDS: 121
SOFTWARE: FASTEST for Windows Version 3.0
SEQ ID NO 93
LENGTH: 706
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-13CKS
US-08-911-824-93

Query Match      89.0%; Score 113; DB 1; Length 706;
Best Local Similarity 81.8%; Pred. No. 2.4e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Cy 1 LLSMCKGKRLVCTSYVQNET 22
11:|||||:|||||:|||||:
Db 618 LLSMCKGKRLVCTSYVQNET 639

RESULT 11
US-08-911-824-91
Sequence 91; Application US/08911824
Publication No. US2003004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sheshi G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165.US.01
CURRENT APPLICATION NUMBER: US/08/911,824
NUMBER OF SEQ IDS: 121
SOFTWARE: FASTEST for Windows Version 3.0
SEQ ID NO 91
LENGTH: 736
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-12CKS
US-08-911-824-91

Query Match      89.0%; Score 113; DB 1; Length 736;
Best Local Similarity 81.8%; Pred. No. 2.5e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Cy 1 LLSMCKGKRLVCTSYVQNET 22
11:|||||:|||||:|||||:
Db 618 LLSMCKGKRLVCTSYVQNET 639

```

```

APPLICANT: Devare, Sheshi G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165.US.01
CURRENT APPLICATION NUMBER: US/08/911,824
NUMBER OF SEQ IDS: 121
SOFTWARE: FASTEST for Windows Version 3.0
SEQ ID NO 61
LENGTH: 873
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: HIV-1 Group O Isolate HAM112
US-08-911-824-61

Query Match      89.0%; Score 113; DB 1; Length 873;
Best Local Similarity 81.8%; Pred. No. 2.9e-08;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Cy 1 LLSMCKGKRLVCTSYVQNET 22
11:|||||:|||||:|||||:
Db 601 LLSMCKGKRLVCTSYVQNET 622

RESULT 13
US-10-026-741-66
Sequence 86; Application US/10026741
Publication No. US20030049604A1
GENERAL INFORMATION:
APPLICANT: CLAVEL, FRANCOISE
APPLICANT: BORMAN, ANDREW
APPLICANT: OUILLENT, CAROLINE
APPLICANT: GUETARD, DENISE
APPLICANT: MONTANIER, LUC
APPLICANT: DONON DE SAINT-MARTIN, JACQUELINE
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pamegan, Henderson, Farbow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
FILING DATE: 27-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/817,441
FILING DATE: 13-Dec-1995
APPLICATION NUMBER: FR 95/01391
FILING DATE: 20-Oct-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-Oct-1994
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-Mar-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

```

INFORMATION FOR SEQ ID NO: 86:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 200 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 86:  
 US-10-026-741-86  
 Query Match 85.8%; Score 109; DB 9; Length 37;  
 Best Local Similarity 81.8%; Pred. No. 5.5e-09;  
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 LLSWGCKGRKLVCTSYVNNKT 22  
 Db 14 LLSWGCKGRKLVCTSYVNNKT 35

RESULT 14  
 Sequence 104, Application US/09854816  
 Patent No. US20020151473A1  
 GENERAL INFORMATION:  
 APPLICANT: Andrew C. Braisted  
 P.O. Kevin Justice  
 J. Christopher Phelan  
 Melissa A. Starovasilk  
 James A. Wells  
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
 NUMBER OF SEQUENCES: 113  
 COMPUTER READABLE FORM:  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/854,816  
 FILING DATE: 15-May-2001  
 PRIOR APPLICATION DATA (Unknown)  
 APPLICATION NUMBER: 08/965,056  
 FILING DATE: (Unknown)  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Torchia, PhD., Timothy E.  
 REGISTRATION NUMBER: 36,700  
 REFERENCE/DOCKET NUMBER: P1005R2  
 TELEPHONE: 650/952-8674  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 104:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 200 amino acids  
 TYPE: Amino Acid  
 STRANDEDNESS: linear  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 104:  
 US-09-854-816-104  
 Query Match 85.8%; Score 109; DB 10; Length 200;  
 Best Local Similarity 81.8%; Pred. No. 2.7e-08;  
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 LLSWGCKGRKLVCTSYVNNKT 22

Db 126 LLSWGCKGRKLVCTSYVNNKT 147  
 RESULT 15  
 US-10-026-741-94  
 Sequence 94, Application US/10026741  
 Publication No. US20030049604A1  
 GENERAL INFORMATION:  
 APPLICANT: CHARNEN, PIERRE  
 P.O. Box 1000  
 BORMAN, ANDREW  
 OUILLET, CAROLINE  
 GUETARD, DENISE  
 MONTAGNIER, LUC  
 DONON DE SAINT-MARTIN, JACQUELINE  
 COHEN, JACQUES  
 TITLE OF INVENTION: NOVEL PEPTIDE SEQUENCES OF HIV-1 TYPE (OR  
 NUMBER OF SEQUENCES: 103  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
 Dunner, L.L.P.  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/026,741  
 FILING DATE: 27-Dec-2001  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/817,441  
 FILING DATE: 31-Aug-1998  
 APPLICATION NUMBER: PCT/FR 95/01391  
 FILING DATE: 20-Oct-92  
 APPLICATION NUMBER: EP 95412554  
 FILING DATE: 20-Oct-1994  
 APPLICATION NUMBER: FR 9502526  
 FILING DATE: 03-Mar-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET INFORMATION: 03260.6005-00000  
 TELEPHONE: 202-408-4400  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 94:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 37 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 94:  
 US-10-026-741-94  
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 Best Local Similarity 72.7%; Pred. No. 1.5e-08;  
 Matches 16; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 LLSWGCKGRKLVCTSYVNNKT 22  
 Db 14 LLSWGCKGRKLVCTSYVNNKT 35  
 Search completed: May 29, 2003, 11:03:56  
 Job time : 19.0317 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:06 / Search time 10.8254 Seconds

(without alignments) 195,370 Million cell updates/sec

Title: US-09-147-362A-3

Sequence: 1 LLSWGCKRGLVCTSYVNNR 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 9613422 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: PIR 73:\*

1: p1r1.\*

2: p1r2.\*

3: p1r3.\*

4: p1r4.\*

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Copy	Length	DB	ID	Description
1	109	85.8	863	2	AS5034		Gag polyprotein -
2	106	83.5	104	2	S52930		GP1 ENV protein -
3	103	81.1	877	2	S49187		envelope protein p
4	84	66.1	854	1	VCLJ81		env polyprotein p
5	83	64	352	2	S22902		envelope protein g
6	82	64	358	2	S22000		envelope protein g
7	82	64.6	358	2	S22000		envelope protein g
8	82	64.6	358	2	S22000		envelope protein g
9	81	63.8	443	2	C41621		env polyprotein p
10	81	63.8	853	2	S54384		envelope polyprote
11	81	63.8	855	1	VCLJ82		env polyprotein pr
12	80	63.0	357	2	S22006		envelope protein g
13	80	63.0	357	2	S22006		envelope protein g
14	80	63.0	357	2	S22006		envelope protein g
15	80	63.0	357	2	S21996		envelope protein g
16	80	63.0	357	2	S21996		envelope protein g
17	80	63.0	358	2	S21998		envelope protein g
18	80	63.0	445	2	A41621		env polyprotein M
19	80	63.0	854	2	B41621		env polyprotein D
20	80	63.0	854	1	VCLJ81		env polyprotein pr
21	80	63.0	854	1	VCLJ81		env polyprotein pr
22	80	63.0	854	1	VCLJ81		env polyprotein pr
23	80	63.0	854	1	VCLJ81		env polyprotein pr
24	80	63.0	854	1	VCLJ81		env polyprotein pr
25	80	63.0	854	1	VCLJ81		env polyprotein pr
26	80	63.0	854	1	VCLJ81		env polyprotein pr
27	80	63.0	854	1	VCLJ81		env polyprotein pr
28	80	63.0	854	1	VCLJ81		env polyprotein pr
29	80	63.0	854	1	VCLJ81		env polyprotein pr

30	80	63.0	859	1	VCLJ8N		env polyprotein pr
31	80	63.0	861	1	VCLJ8V		env polyprotein pr
32	80	63.0	861	1	VCLJ8V		env polyprotein pr
33	80	63.0	868	1	VCLJ84		env polyprotein pr
34	79	62.2	786	2	S28084		env polyprotein -
35	78.5	61.8	855	2	A45713		env transmembrane
36	78	61.4	856	2	A44963		env polyprotein pr
37	77	60.6	846	1	VCLJND		env polyprotein pr
38	74.5	58.7	859	1	VCLJST		env polyprotein pr
39	74.5	58.7	859	1	VCLJST		env polyprotein pr
40	74.5	58.7	859	1	VCLJST		env polyprotein pr
41	74.5	58.7	859	1	VCLJST		env polyprotein pr
42	74	58.3	729	1	VCLJKB		env protein - simi
43	74	58.3	861	1	VCLJKB		env polyprotein pr
44	73	57.5	851	2	S33985		env polyprotein pr
45	72.5	57.1	151	2	S30448		env protein - huma

## ALIGNMENTS

RESULT 1  
Gag polyprotein - human immunodeficiency virus type 1 (strain Ant70)

C:Species: human immunodeficiency virus type 1, HIV-1, HXB-2, change 07-May-1999

C:Accession: A53034

R:Vanden Haesevelde, M.; Decourt, J.L.; De Lays, R.J.; Vanderborgh, B.; van der Groen, J. Virol. 68, 1586-1596, 1994

A:Title: Genomic cloning and complete sequence analysis of a highly divergent African hu

A:Accession number: A53034; PMID:8107220

A:Status: preliminary

A:Residues: 1863 (YVNV)

A:Cross-references: GB:102587

A:Superfamily: type B retrovirus env polyprotein

C:Keywords: polyprotein

Query Match

Best Local Similarity 85.84; Score 109; DB 2; Length 863;

Matches 18; conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 594 LLSWGCKRGLVCTSYVNNR 615

1 LLSWGCKRGLVCTSYVNNR 22

594 LLSWGCKRGLVCTSYVNNR 615

RESULT 2

GP1 ENV protein - human immunodeficiency virus type 1 (Fragrant)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Accession: S52930

R:Vanden Haesevelde, M.; Decourt, J.L.; De Lays, R.J.; Vanderborgh, B.; van der Groen, J. Virol. 68, 1586-1596, 1994

A:Title: Genomic cloning and complete sequence analysis of a highly divergent African hu

A:Accession number: S52930

A:Status: preliminary

A:Residues: 1863 (YVNV)

A:Cross-references: EMBL:X84328; NID:965526; PID:CA59066.1; PID:965527

C:Superfamily: type B retrovirus env polyprotein

Query Match

Best Local Similarity 83.54; Score 106; DB 2; Length 104;

Matches 16; conservative 4; Mismatches 2; Indels 0; Gaps 0;

DB 1 LLSWGCKRGLVCTSYVNNR 22

45 LLSWGCKRGLVCTSYVNNR 66



C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 12-Apr-1995  
 C:Accession: S22000  
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 Submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi  
 A:Reference number: S21990  
 A:Accession: S22000  
 A:Status: preliminary  
 A:Molecule type: RNA  
 A:Residues: 1358 <STR>  
 A:Cross-references: EMBL:X61351  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 64.6%; Score 82; DB 2; Length 358;  
 Best Local Similarity 65.0%; Pred. No. 0.00031;  
 Matches 12; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTGVNNR 20  
 |||||:|||||:  
 94 LGLTIGSGKRLCTTVPMNN 113

RESULT 8  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Accession: gp120/GP41 - human immunodeficiency virus type 1 (patient 3B) (fragment  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: patient 3B  
 C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 26-Aug-1999  
 C:Accession: S70417  
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Description: Distinct populations of human immunodeficiency virus type 1 in blood and cereb  
 A:Reference number: A26192; NCID:87246097; PMID:17936740  
 A:Accession: S70417  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1358 <STR>  
 A:Cross-references: EMBL:X61351; NID:G60184; PIDN:CAA43514.1; PID:G60185  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 64.6%; Score 82; DB 2; Length 358;  
 Best Local Similarity 65.0%; Pred. No. 0.00031;  
 Matches 12; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTGVNNR 20  
 |||||:|||||:  
 94 LGLTIGSGKRLCTTVPMNN 113

RESULT 9  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Accession: P - human immunodeficiency virus type 1 (fragment)  
 A:Alternate names: coat polyprotein  
 N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C>Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
 C:Accession: C41621  
 R: Burger, H.; Weiser, B.; Flaherty, K.; Galla, J.; Nguyen, P.N.; Gibbs, R.A.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 1126-11240, 1991  
 A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
 A:Reference number: A41621; NCID:92107924; PMID:1763038  
 A:Accession: C41621  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1544 <STR>  
 A:Cross-references: GB:M77230; NID:G32863; PIDN:AAA03792.1; PID:G55015  
 A>Note: this virus was isolated from the mother's sexual partner  
 C:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Accession: gp120/GP41 - human immunodeficiency virus type 1 (patient 3B) (fragment  
 F:252-443/Product: coat protein gp41 (fragment) #status predicted <STR>

F:424-443/Domain: transmembrane #status predicted <TM>  
 F:79-123,36,46,78,101,107,131,137,143,147,153,168,200,203,351,356,365,377/Binding site: ca  
 Query Match 63.8%; Score 81; DB 2; Length 443;  
 Best Local Similarity 54.5%; Pred. No. 0.00053;  
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTGVNNR 22  
 |||||:|||||:  
 332 LGLTIGSGKRLCTTVPMNNS 353

RESULT 10  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Accession: S54384  
 A:Status: preliminary  
 A:Molecule type: genomic RNA  
 A:Residues: 1853 <TR>  
 A:Cross-references: EMBL:MP2639; NID:G329377; PIDN:AAA45370.1; PID:G329385  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: polyprotein

Query Match 63.8%; Score 81; DB 2; Length 853;  
 Best Local Similarity 54.5%; Pred. No. 0.00093;  
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTGVNNR 22  
 |||||:|||||:  
 589 LGLTIGSGKRLCTTVPMNNS 610

RESULT 11  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Accession: P - human immunodeficiency virus Zr-6  
 A:Alternate names: coat polyprotein  
 N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
 C:Species: human immunodeficiency virus Zr-6  
 C>Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999  
 C:Accession: D26192  
 R: Srinivasan, A.; Amand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochman, G.; Cu  
 Gene 52, 71-82, 1987  
 A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti  
 A:Reference number: A26192; NCID:87246097; PMID:303660  
 A:Accession: D26192  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1855 <STR>  
 A:Cross-references: GB:M16322; NID:G329398; PIDN:AAA45380.1; PID:G329403  
 C:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Accession: gp120/GP41 - human immunodeficiency virus type 1 (patient 3B) (fragment  
 F:20-855/Product: env polyprotein #status predicted <STR>  
 F:20-855/Product: env polyprotein #status predicted <STR>  
 F:501-855/Product: transmembrane glycoprotein #status predicted <TM>  
 F:87-123,140,145,154,158,169,199,236,243,266,278,291,297,333,340,355,366,392,398,404

Query Match 63.8%; Score 81; DB 1; Length 855;  
 Best Local Similarity 54.5%; Pred. No. 0.00093;  
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTGVNNR 22  
 |||||:|||||:  
 591 LGLTIGSGKRLCTTVPMNNS 612

RESULT 12

```

522006
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 26-Aug-1999
C:Accession: S22004
A:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70420
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STE2>
A:Cross-references: EMBL:X61354; NID:g60190; PIDN:CAA43620.1; PID:g60191
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polypeptide

Query Match
at Local Similarity 63.0%; Score 80; DB 2; Length 357;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Cy 1 LLSNGCGKGRVCTYSVQWN 20
Db 93 LGLWGSGSKRLCTTAVPWN 112

RESULT 13
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 01-Dec-2000
C:Accession: S21994; S70421
A:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S21994
A:Reference number: S21990
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180
A:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140; X', 142-312; X', 314-357 <STE2>
A:Cross-references: EMBL:X61355; NID:g60179
C:Superfamily: type E retrovirus env polypeptide

Query Match
at Local Similarity 63.0%; Score 80; DB 2; Length 357;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Cy 1 LLSNGCGKGRVCTYSVQWN 20
Db 93 LGLWGSGSKRLCTTAVPWN 112

RESULT 14
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 01-Dec-2000
C:Accession: S22004; S70419
A:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S21990
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180
A:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140; X', 142-312; X', 314-357 <STE2>
A:Cross-references: EMBL:X61355; NID:g60179
C:Superfamily: type E retrovirus env polypeptide

Query Match
at Local Similarity 63.0%; Score 80; DB 2; Length 357;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Cy 1 LLSNGCGKGRVCTYSVQWN 20
Db 93 LGLWGSGSKRLCTTAVPWN 112

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A:Accession: S22004
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61353; NID:g60188; PIDN:CAA43618.1; PID:g60189
A:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70419
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-292; X', 294-357 <STE2>
A:Cross-references: EMBL:X61356; NID:g60188
C:Superfamily: type E retrovirus env polypeptide

Query Match
at Local Similarity 63.0%; Score 80; DB 2; Length 357;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Cy 1 LLSNGCGKGRVCTYSVQWN 20
Db 93 LGLWGSGSKRLCTTAVPWN 112

RESULT 15
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 26-Aug-1999
C:Accession: S21996
A:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70422
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STE2>
A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polypeptide

Query Match
at Local Similarity 63.0%; Score 80; DB 2; Length 357;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Cy 1 LLSNGCGKGRVCTYSVQWN 20
Db 93 LGLWGSGSKRLCTTAVPWN 112

Search completed: May 29, 2003, 10:40:22
Job time : 10.8254 secs

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DR HIV; K03458; ENV556; Env GP41.  
 DR HIV; P00003; GP120.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR AIDS; Coat protein; Glycoprotein; Transmembrane;  
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 FT CHAIN 31 60  
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 Db 591 LLSWGCKGRVLCYSYQVNER 612  
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 AC P33561;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [contamin: Exterior membrane  
 glycoprotein (GP160), Transmembrane glycoprotein (GP161)].  
 OS Human immunodeficiency virus type 1 (YO-2 isolate) (HIV-1).

CC HIV; K03458; ENV556; Env GP41.  
 CC HIV; P00003; GP120.  
 CC InterPro: IPR000777; GP120.  
 CC Pfam: PF00516; GP120; 1.  
 CC AIDS; Coat protein; Glycoprotein; Transmembrane;  
 signal.  
 FT SIGNAL 1 29  
 FT CHAIN 30 489  
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 Local 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
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 Db 591 LLSWGCKGRVLCYSYQVNER 612  
 RESULT 4  
 ENV\_HYV2 STANDARD; PRT; 843 AA.  
 AC P33561;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [contamin: Exterior membrane  
 glycoprotein (GP160), Transmembrane glycoprotein (GP161)].  
 OS Human immunodeficiency virus type 1 (YO-2 isolate) (HIV-1).

[illegible]





BX MEDLINE=99085613; PubMed=2198516;  
 RA Arand R., Thayer R., Schinweean A., Naylor S., Gardner M., Luciw P.,  
 RA Dandekar S.;  
 RT "Biological and molecular characterization of human immunodeficiency  
 RT virus (HIV-1BR) from the brain of a patient with progressive  
 RT dementia";  
 RT Virology 268:68-79, 1999.  
 CC 1- HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.  
 CC -----  
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 CC -----  
 CC EMBL, M21098; AAC44221.1; -  
 CC PIR; A31667; VCUJBR.  
 CC HIV; M21098; ENVISERVA  
 CC InterPro: IPR000779; GP120.  
 CC Pfam; PF00516; GP120; 1.  
 CC DR Pfam; PF00517; GP11; 1.  
 CC KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 CC Signal.  
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 CC FT CHAIN 31 507  
 CC FT CHAIN 51 507  
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 CC FT DISULFID 119 205  
 CC FT DISULFID 126 196  
 CC FT DISULFID 131 155  
 CC FT DISULFID 218 247  
 CC FT DISULFID 228 239  
 CC FT DISULFID 376 439  
 CC FT DISULFID 383 412  
 CC FT CARBOHYD 48 49  
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 Matches 12; Conservative 3; Mismatch 5; Indels 0; Gaps 0;

CC MEDLINE=99085613; PubMed=2198516;  
 CC RA Arand R., Thayer R., Schinweean A., Naylor S., Gardner M., Luciw P.,  
 CC RA Dandekar S.;  
 CC RT "Biological and molecular characterization of human immunodeficiency  
 CC RT virus (HIV-1BR) from the brain of a patient with progressive  
 CC RT dementia";  
 CC RT Virology 268:68-79, 1999.  
 CC CC 1- HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.  
 CC CC -----  
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 CC CC use by non-profit institutions as long as its content is in no way  
 CC CC entitles requires a license agreement. Usage by and for commercial/  
 CC CC or send an email to license@db.slb.ch).  
 CC CC -----  
 CC CC EMBL, M21098; AAC44221.1; -  
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 CC CC HIV; M21098; ENVISERVA  
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 CC CC FT CHAIN 31 507  
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 FT CARBOHYD 812 812 N-LINKED (GLCNAC.. ) (POTENTIAL).  
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 Best Local Similarity 60.0%; Pred. No. 0.00014;  
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 1 LLSMGGCKRKYCTSYVNM 20  
 588 LLSMGGCKRKYCTSYVNM 607  
 RESULT 10  
 ID ENV HYLMF STANDARD; PRT; 853 AA.  
 AC P19531;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DT Envelope polypeptide gp160 precursor [contains: Exterior membrane  
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 DB Envelope polypeptide gp160 precursor [contains: Exterior membrane  
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).  
 OC Viruses; Retroviridae; Lentivirus.  
 NCBI TaxID=11704;  
 [1]  
 RX SEQUENCE FROM N.A.  
 RA REGIONS=5037877; PubMed=1693284;  
 RA REGIONS=5037877; PubMed=1693284;  
 RA Weisak A., Haggerty S., Lamont C., Mann A.M., Meyer C.,  
 RT "Cloning and characterization of human immunodeficiency virus type 1  
 RT variants diminished in the ability to induce syncytium-independent  
 RT cytolysis.";  
 RL J. Virol. 64:3792-3803(1990).  
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 CC -----  
 CC EMBL: M3381; GI: 503150.1;  
 CC EMBL: M3381; GI: 503150.1;  
 CC HIV: M3343; ENVSWP;  
 DR InterPro: IPR000128; Env GP41.  
 DR InterPro: IPR000128; Env GP41.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00516; GP120; 1.  
 KM AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 RT Signal.  
 FT CHAIN 1 30  
 FT CHAIN 510 509 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 54 74 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFD 119 203 BY SIMILARITY.  
 FT DISULFD 126 194 BY SIMILARITY.  
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FT DISULFD 383 416 BY SIMILARITY.  
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 SQ SEQUENCE 853 AA; 96912 MW; 3377B93B6F22BA CRC64;  
 Query Match 63.0%; Score 80; DB 1; Length 853;  
 Best Local Similarity 60.0%; Pred. No. 0.00014;  
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 1 LLSMGGCKRKYCTSYVNM 20  
 590 LLSMGGCKRKYCTSYVNM 609  
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 ID ENV HYLMF STANDARD; PRT; 855 AA.  
 AC P03378;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DT Envelope polypeptide gp160 precursor [contains: Exterior membrane  
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 DB Envelope polypeptide gp160 precursor [contains: Exterior membrane  
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 OS Human immunodeficiency virus type 1 (HIV/SF isolate) (HIV-1).  
 OC Viruses; Retroviridae; Lentivirus.  
 NCBI TaxID=11695;  
 [1]  
 RX SEQUENCE FROM N.A.  
 RA REGIONS=5090453; PubMed=2578227;  
 RA REGIONS=5090453; PubMed=2578227;  
 RA Streptom M.M., Brown S.M., Goe W.M., Reinhard A.S.,  
 RA Levy J.A., Dina P., Luciw P.A., Gee W.M., Reinhard A.S.,  
 RT "Nucleotide sequence and expression of an AIDS-associated retrovirus  
 RT (ARV-2)."  
 RL Science 227:484-492(1985).  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: K02007; AB05982.1;

DR FIR: A03576; VCLJ2.  
 DR HIV: K02001; J03552.  
 DR D1: J03552; ENV GP41.  
 DR InterPec: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 29  
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 SQ  
 Query Match 63.0%; Score 80; DB 1; Length 855;  
 Best Local Similarity 60.0%; Pred. No. 0.0014;  
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
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 DB 591 LLSWGCKRSLVCTSYVM 610  
 RESULT 12  
 ENV HYLOY STANDARD; PRT; 855 AA.  
 ID ENV HYLOY  
 AC P20688;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DE Envelope glycoprotein GP120 precursor (Contains: Exterior membrane  
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)).  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).

CC HIVuses; Retroid viruses; Retroviridae; Lentiviruses.  
 CC NCBI\_TaxId=11599;  
 RN SEQUENCE FROM N.A.  
 RA MEDLINE=9014544; Pubmed=2559749;  
 RA Huot T.; Dazza M.C.; Brun-Vezinet P.; Roelants G.E.; Main-Hobson S.;  
 RA "A highly defective HIV-1 strain isolated from a healthy gibbon  
 RT individual presenting an atypical western blot."  
 RT AIDS; MISCLEANDERS; THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A  
 CC "HEALTHY GIBBON INDIVIDUAL."  
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 CC  
 DR EMBL: M26727; AA08397.1; -  
 DR HIV: M26727; ENV GP41.  
 DR InterPec: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 510 855  
 FT DISULFID 53 73  
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 Best Local Similarity 60.0%; Pred. No. 0.0014;  
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Page 9

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FT	CARBOHYD	234	234	N-LINKED	(GLCNAC .)
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FT	CARBOHYD	262	262	N-LINKED	(GLCNAC .)
FT	CARBOHYD	269	269	N-LINKED	(GLCNAC .)
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FT	CARBOHYD	385	386	N-LINKED	(GLCNAC .)
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FT	CARBOHYD	674	674	N-LINKED	(GLCNAC .)
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FT	CARBOHYD	816	816	N-LINKED	(GLCNAC .)
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Query Match		63.0%;	Score 80;	DB 1;	Length 856;
Beech Local Similarity		60.0%;	Fred; N.0.0014;		
Matched 12;	Conservative	3;	Mismatches	5;	Gaps 0.
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Db	592 LLGIWGCSGKLCTVAPWN 611				
RESULT 14					
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AC P04578; C09779;					
DT 13-AUG-1987 (Rel. 05; Created)					
DT 15-JUL-1999 (Rel. 38; Last sequence update)					
DT 30-MAY-2000 (Rel. 39; Last annotation update)					
DT Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP20); Transmembrane glycoprotein (GP11)].					
DE HIV immunodeficiency virus type 1 (HRX2 isolate) (HIV-1).					
CC Virus[es]. Retrov[ir]idae; Retroviridae; Lentivirinae.					
OC NCBI_TaxID=11706;					
NCBI TaxID=11706;					
[1]					
R.P. SEQUENCE FROM N.A.					
R.X MEDLINE-87299196; PubMed-3040055;					
R.R Retner L., Fishner A., Jagodzinski L.L., Miteuya H., Liou R.-S., Gaillo R.C., Wong-Staal F.;					
R.T "The nucleotide sequences of functional clones of the AIDS AIDS Res. Hum. Retroviruses 3:57-69(1987).					
RL [2]					
RP REVISIONS.					
RA Retner L., Fishner A., Jagodzinski L.L., Miteuya H., Liou R.-S., Gaillo R.C., Wong-Staal F.;					
RA Submitted (Apr-1997) to the EMBL/Genebank/DBJ databases.					
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EMBL: K03455; AF060702.1					

OC		Human Immunodeficiency Virus Type 1 (WU-75 isolate) (HIV-1).
CC	Viruses; Retroviridae; Lentivirinae.	
RA	NB01_TaxID=82894.	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE:95127297; PubMed:7626699;	
RA	Ratiz M.S., Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M., Shaw G.N., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Baltimore W.;	
RT	Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (sequences 10-1178-1155)(1994).	
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CC	EMBL: U12055; AAA76690.1.	
DR	Glycosylated; Q706265; ENV_GP41.	
DR	InterPro: IPRO03028; ENV_GP41.	
DR	InterPro: IPRO00777; GP120.	
DR	Pfam: PF00516; GP120_1.	
KM	Fam: P00517; GP41; Transmembrane protein; glycoprotein; Glycoprotein; Transmembrane signal.	
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FT	PT CHAIN 512 856	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID 54 307A	BY SIMILARITY.
FT	DISULFID 112 156	BY SIMILARITY.
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FT	DISULFID 228 239	BY SIMILARITY.
FT	DISULFID 296 331	BY SIMILARITY.
FT	DISULFID 378 445	BY SIMILARITY.
FT	DISULFID 388 468	BY SIMILARITY.
FT	CARBOHYD 136 136	N-LINKED (GLCNAC . ) (POTENTIAL).
FT	CARBOHYD 141 141	N-LINKED (GLCNAC . ) (POTENTIAL).
FT	CARBOHYD 156 156	N-LINKED (GLCNAC . ) (POTENTIAL).
FT	CARBOHYD 160 160	N-LINKED (GLCNAC . ) (POTENTIAL).
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FT	CARBOHYD 397 397	N-LINKED (GLCNAC . ) (POTENTIAL).
FT	CARBOHYD 406 406	N-LINKED (GLCNAC . ) (POTENTIAL).
FT	CARBOHYD 443 443	N-LINKED (GLCNAC . ) (POTENTIAL).
FT	CARBOHYD 611 611	N-LINKED (GLCNAC . ) (POTENTIAL).
FT	CARBOHYD 616 616	N-LINKED (GLCNAC . ) (POTENTIAL).
FT	CARBOHYD 624 624	N-LINKED (GLCNAC . ) (POTENTIAL).
FT	CARBOHYD 637 637	N-LINKED (GLCNAC . ) (POTENTIAL).
FT	CARBOHYD 674 674	N-LINKED (GLCNAC . ) (POTENTIAL).
FT	CARBOHYD 730 730	N-LINKED (GLCNAC . ) (POTENTIAL).
FT	CARBOHYD 810 810	N-LINKED (GLCNAC . ) (POTENTIAL).
SC	SEQUENCE 856 AA; 96938 MW; OC41332CF7E6687 CRC64;	

Query Match 63.04; Score 90; DB 1; Length 856;  
Seq. Identity 63.04; Read No. 0.00014;  
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 1 LLSMGCGRIVCYSYOWN 20  
DB 592 LGGMGCSKLICTTAVPWN 611

Search Completed: May 29, 2003, 10:36:58  
Job time: 5.4127 secs

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AC 09166;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DB Env polypeptide, gp41 (Fragment).
DB Env. Immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11676;
NM [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BCP107;
RA Riquens P., Robertson D., Diamond F., Souquiere S., Mauciere P.,
RA "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.",
RA Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AJ234604; CAB6250.1;
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; GP41; 1.
DB Transmembrane.
FT NON_TER 1
FT NON_TER 203
SQ SEQUENCE 209 AA; 24116 MW; 91AC9B2BFF7A9B3 CRC64;
Query Match 91.3%; Score 116; DB 15; Length 209;
Best Local Similarity 86.4%; Pred. No. 3,8e-10;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Oy 1 LLSMCKGRIVCYTSVQNNET 22
Db 56 LLSMCKGRIVCYTSVQNNET 77

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RESULT 3
O9166 PRELIMINARY; PRT; 219 AA.
AC 09166;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DB Env polypeptide, gp41 (Fragment).
DB Env. Immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11676;
NM [1]
RP SEQUENCE FROM N.A.
RA Riquens P., Robertson D., Sandrine S., Chistrel D., Francois S.,
RA "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.",
RA Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AJ234604; CAB6250.1;
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; GP41; 1.
DB Transmembrane.
FT NON_TER 1
FT NON_TER 219
SQ SEQUENCE 219 AA; 28353 MW; F65629E0152091 CRC64;
Query Match 90.6%; Score 115; DB 15; Length 219;
Best Local Similarity 86.4%; Pred. No. 5,7e-10;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Oy 1 LLSMCKGRIVCYTSVQNNET 22
Db 57 LLSMCKGRIVCYTSVQNNET 78

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DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DB Envelope transmembrane glycoprotein (Fragment).
DB Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11676;
NM [1]
RP SEQUENCE FROM N.A.
RA BIPOLLET-RUCHE F., KRAE E., PEETERS M., DELAPORTE E.;
RA "Molecular characterization of envelope transmembrane glycoprotein of
RA 14 new human immunodeficiency virus type 1 group O strains from
RA different African countries.",
RA Submitted (Dec-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF228237; NAF1914.1;
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; GP41; 1.
DB Transmembrane.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 13865 MW; 540F5B5F7AD849D8 CRC64;
Query Match 89.0%; Score 113; DB 15; Length 116;
Best Local Similarity 81.8%; Pred. No. 6,2e-10;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Oy 1 LLSMCKGRIVCYTSVQNNET 22
Db 39 LLSMCKGRIVCYTSVQNNET 60

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RESULT 5
O91H07 PRELIMINARY; PRT; 124 AA.
AC 091H07;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DB Envelope glycoprotein (Fragment).
DB GP41.
OC Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11676;
NM [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20386754; Pubmed=10933623;
RA Yang C., Gao F., Fonjuncq P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lai R.B.;
RA "Phylogenetic analysis of protease and transmembrane regions of HIV
RA type 1 group O.",
RA Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF228237; NAF1914.1;
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; GP41; 1.
DB Transmembrane.
FT NON_TER 1
FT NON_TER 124
SQ SEQUENCE 124 AA; 15187 MW; 105D515F114450F8 CRC64;
Query Match 89.0%; Score 113; DB 15; Length 124;
Best Local Similarity 81.8%; Pred. No. 6,6e-10;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Oy 1 LLSMCKGRIVCYTSVQNNET 22
Db 33 LLSMCKGRIVCYTSVQNNET 54

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RESULT 4
O40458 PRELIMINARY; PRT; 116 AA.
ID O40458;
AC O40458;

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RESULT 6
O91H09 PRELIMINARY; PRT; 130 AA.
ID O91H09

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AC 091HB9;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CM798;
RA MEDLINE=20386754; PubMed=10931623;
RQ Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,
RA Pientazek D., Schable C., Lai R.B.;
RL Phylogenetic analysis of and transmembrane regions of HIV
RT Envelope glycoprotein (Fragment).
RM AIDS Ref22935; AAF1912.1;
DR EMBL; AF22935; AAF1912.1;
PFam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT TER 130
SQ SEQUENCE 130 AA; 15593 MW; 5385769A336344RA CRC64;

Query Match
Best Local Similarity 89.0%; Score 113; DB 15; Length 130;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LLSWGCKGRILCYTSVKNNT 22
Db 40 LLSWGCKGRILCYTSVKNNT 61

RESULT 7
O91B95 PRELIMINARY; PRT; 218 AA.
ID O91B95;
AC O91B95;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF5;
RA Rognes P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RL "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
RT Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
RM InterP: IPR000328; ENV_GP41.
DR EMBL; AJ13062; CAB6223.1;
DR InterP: IPR000328; ENV_GP41.
PFam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT TER 218
SQ SEQUENCE 218 AA; 25243 MW; E7F0E1E30EF79FA8 CRC64;

Query Match
Best Local Similarity 89.0%; Score 113; DB 15; Length 218;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Cy 1 LLSWGCKGRILCYTSVKNNT 22
Db 54 LLSWGCKGRILCYTSVKNNT 75

RESULT 8
O91B82

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ID O91B82 PRELIMINARY; PRT; 230 AA.
AC O91B82;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF15;
RA Rognes P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RL "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
RT Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
RM InterP: IPR000328; ENV_GP41.
DR EMBL; AJ13062; CAB6223.1;
DR InterP: IPR000328; ENV_GP41.
PFam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT TER 230
SQ SEQUENCE 230 AA; 26705 MW; C1F74482P51302D CRC64;

Query Match
Best Local Similarity 89.0%; Score 113; DB 15; Length 230;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Cy 1 LLSWGCKGRILCYTSVKNNT 22
Db 55 LLSWGCKGRILCYTSVKNNT 76

RESULT 9
O91B85 PRELIMINARY; PRT; 536 AA.
ID O91B85;
AC O91B85;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE ENV polypeptide (fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF15;
RA Rognes P., Robertson D., Dawson F., Souquiere S., Mauciere P.,
RA Delenne C., Brun-Vezinet F., Dormont D.;
RL "HIV-1 group O phylogenetic analysis of C2-GP41 region.";
RT Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
RM InterP: IPR000328; ENV_GP41.
DR EMBL; AJ13062; CAB6223.1;
DR InterP: IPR000328; ENV_GP41.
PFam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT TER 536
SQ SEQUENCE 536 AA; 60419 MW; CF531BAAF0B8E52 CRC64;

Query Match
Best Local Similarity 89.0%; Score 113; DB 15; Length 536;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Cy 1 LLSWGCKGRILCYTSVKNNT 22
Db 361 LLSWGCKGRILCYTSVKNNT 382

RESULT 10
O91B82

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[illegible]

Page 5

Matches	18; Conservative	4; Mismatches	0; Indels	0; Gaps	0;
Qy	1	LLSSGCKGRLLVCYTSVNKKNT	22		
		:     :     : :			
Db	618	LLSSGCKGRLLVCYTSVNKKNT	639		

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Job time : 22.6984 secs

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GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: May 29, 2003, 10:30:20 / Search time 29.3333 Seconds

(without alignments)  
99.938 Million cell updates/sec

Title: US-09-147-362a-4

Perfect score: 126

Sequence: 1 LUSMCKGKGLVCTYSVMNST 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126	100.0	22	19	AAAB0462
2	122	96.8	22	19	AAAB0461
3	122	96.8	22	19	AAAB0463
4	122	96.8	22	19	AAAB0466
5	115	91.3	42	13	AAAB0460
6	113	89.7	22	19	AAAB0465
7	113	89.7	40	17	AAAB0464
8	112	88.9	32	19	AAAB0469
9	112	88.9	41	17	AAAB0751
10	112	88.9	113	20	AAV05565

11	112	88.9	715	20	AAV05525	HIV-1 group O f001
12	111	88.1	33	21	AAH12212	Partial sequence o
13	111	88.1	113	20	AAV05559	HIV-1 group O f001
14	110	87.3	33	21	AAH12231	Partial sequence o
15	110	87.3	40	17	AAAB07343	Partial sequence o
16	110	87.3	40	17	AAAB07344	Partial sequence o
17	110	87.3	41	17	AAAB07345	Partial sequence o
18	110	87.3	117	20	AAV05548	HIV-1 group O f001
19	109	86.5	116	20	AAV05555	HIV-1 group O f001
20	108	85.7	22	19	AAAB0464	Peptide derived fr
21	108	85.7	22	19	AAAB0465	Peptide derived fr
22	108	85.7	23	20	AAV05523	Partial sequence o
23	108	85.7	23	21	AAH12236	Partial sequence o
24	108	85.7	43	17	AAH12238	Partial sequence o
25	108	85.7	113	20	AAV05551	HIV-1 group O f001
26	108	85.7	113	20	AAV05550	HIV-1 group O f001
27	108	85.7	139	19	AAAB09318	Anti-HIV-1 group O
28	108	85.7	139	21	AAU72558	Anti-HIV-1 group O
29	108	85.7	150	19	AAAB09319	Anti-HIV-1 group O
30	108	85.7	150	21	AAU72559	Anti-HIV-1 group O
31	108	85.7	150	21	AAU72560	Anti-HIV-1 group O
32	108	85.7	200	21	AAU72578	Anti-HIV-1 group O
33	108	85.7	200	23	ABG68379	Recombinant pCO-8P
34	108	85.7	215	20	AAV09499	HIV-1 group O env
35	108	85.7	215	20	AAV06983	Recombinant pCO-8P
36	108	85.7	215	21	AAV73774	HIV-1 group O env
37	108	85.7	245	20	AAV09493	HIV-1 group O env
38	108	85.7	245	20	AAV06977	Recombinant pCO-3P
39	108	85.7	281	20	AAV09507	HIV-1 group O env
40	108	85.7	281	20	AAV09507	HIV-1 group O env
41	108	85.7	373	20	AAV09495	Recombinant pCO-11
42	108	85.7	373	20	AAV09500	HIV-1 group O env
43	108	85.7	460	20	AAV06984	Recombinant pCO-8C
44	108	85.7	460	20	AAV73755	HIV-1 group O env
45	108	85.7	460	21	AAV73755	HIV-1 group O env

# ALIGNMENTS

RESULT 1  
AAAB0462  
ID AAAB0462 standard; peptide; 22 AA.  
AC AAAB0462;  
XX  
XX 28-JUN-1999 (first entry)  
DT  
XX Peptide derived from a conserved sequence of group O human HIV.  
XX  
XX Group O human immune deficiency virus, HIV, detection: infection.  
XX  
XX Synthetic.  
OS  
XX Immune deficiency virus.  
XX  
XX W09845321-A1.  
XX  
XX 15-OCT-1998.  
XX  
XX 06-APR-1998; 98MO-FR00691.  
XX  
XX 24-FEB-1998; 98FR-0002212.  
XX  
XX 09-APR-1997; 97FR-0004356.  
XX  
XX (SNP ) PASTERIS SANOPI DIAGNOSTICS SA.  
XX  
XX Cheneboux DMb, Delagrange JFH, Godelle SIX, Rieunier FY;  
XX WPI; 1996-58190/49.  
XX  
XX New synthetic peptide(s) - useful for e.g. detecting infection by  
XX human immune deficiency virus of group O

PS Claim 6; Page 42; 55pp; French.  
 XX AA0465-74 represent synthetic peptides (either linear or cyclized by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 XX

Sequence 22 AA;

Query Match 100.0%; Score 126; DB 19; Length 22;

Best Local Similarity 100.0%; Pred. No. 8.2e-10; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 LLSMCKGRIVCTYSVQNMST 22  
 1 LLSMCKGRIVCTYSVQNMST 22

BLT 2

ID AA0461 standard; peptide; 22 AA.

AA0461;

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

WO9845323-A1.

15-OCT-1998.

06-APR-1998; 98MO-FR00691.

24-FEB-1998; 98FR-0002312.

09-APR-1997; 97FR-0004356.

(SNP1) PASTEUR SANOFI DIAGNOSTICS SA.

Cheneboux DMB, Delagrange JFH, Gabelle SIX, Rieunier FY;

WPI; 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by  
 human immune deficiency virus of group O

Claim 6; Page 42; 55pp; French.

AA0465-74 represent synthetic peptides (either linear or cyclized by  
 Cys-Cys disulphide bonds). The peptides represent variable sequences  
 connected around short highly conserved sequences present in isolates  
 of group O human immune deficiency virus (HIV). The peptides are  
 useful as immunological reagents for detecting infection by group O  
 human immune deficiency virus (HIV).

Sequence 22 AA;

Query Match 96.8%; Score 122; DB 19; Length 22;

Best Local Similarity 95.5%; Pred. No. 8.2e-09; Mismatches 1; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 LLSMCKGRIVCTYSVQNMST 22  
 1 LLSMCKGRIVCTYSVQNMST 22

RESULT 3

ID AA0463 standard; peptide; 22 AA.

AA0463;

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

WO9845323-A1.

15-OCT-1998.

06-APR-1998; 98MO-FR00691.

24-FEB-1998; 98FR-0002312.

09-APR-1997; 97FR-0004356.

(SNP1) PASTEUR SANOFI DIAGNOSTICS SA.

Cheneboux DMB, Delagrange JFH, Gabelle SIX, Rieunier FY;

WPI; 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by  
 human immune deficiency virus of group O

Claim 6; Page 42; 55pp; French.

AA0465-74 represent synthetic peptides (either linear or cyclized by  
 Cys-Cys disulphide bonds). The peptides represent variable sequences  
 connected around short highly conserved sequences present in isolates  
 of group O human immune deficiency virus (HIV). The peptides are  
 useful as immunological reagents for detecting infection by group O  
 human immune deficiency virus (HIV).

Sequence 22 AA;

Query Match 96.8%; Score 122; DB 19; Length 22;

Best Local Similarity 95.5%; Pred. No. 2.7e-09; Mismatches 1; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 LLSMCKGRIVCTYSVQNMST 22  
 1 LLSMCKGRIVCTYSVQNMST 22

RESULT 4

ID AA0466 standard; peptide; 22 AA.

AA0466;

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

WO9845323-A1.

15-OCT-1998.

06-APR-1998; 98MO-FR00691.



XX 24-FEB-1998: 98FR-0002212.  
 PR 09-APR-1997: 97FR-0004356.  
 XX (SNFI ) PASTERIS SANOFI DIAGNOSTICS SA.  
 XX Chenebaux DMB, Delagneau JFH, Gabelle SIX, Rieunier FY;  
 XX WPI, 1998-583190/49.  
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by  
 PT human immune deficiency virus of group O  
 XX Claim 6; Page 43; 55pp; French.  
 XX  
 XX AA80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds) which represent variable sequences  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 S0 Sequence 22 AA;  
 Query Match 94.4%; Score 119; DB 19; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 6, 7e-09;  
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 LLSNGCKGRILVCYSYVQNST 22  
 Db 1 LLSNGCKGRILVCYSYVQNST 22  
 1 LLSNGCKGRILVCYSYVQNST 22  
 RESULT 5  
 ID AA007346  
 AC AA007346 standard; peptide; 40 AA.  
 XX AA007346;  
 DT 03-JUN-1997 (first entry)  
 DE Partial sequence of gp41 from HIV-1 gp. O strain BCF07 (MAN).  
 XX Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;  
 XX gp120-env; gp41; gag; penv; strain; gp120; hypervariable loop;  
 XX p12env; p12env; p12env; amplification; PCR; polymerase chain reaction;  
 KM immunogen; antibody.  
 KM Human immunodeficiency virus type 1.  
 EN W05627013-A1.  
 XX 06-SEP-1996.  
 XX 26-FEB-1996: 96MO-FR00294.  
 PR 27-FEB-1995: 95FR-0002236.  
 XX (ASSI-) ASSISTANCE PUBLIQUE HOPITALX PARIS.  
 XX (INRA) INSERM INST NAT SANTE & RECH MEDICALE.  
 PI Chaux-Baudier ML, Lousselet-Ajaka I, Ly T, Saragosti S, Simon F;  
 XX WPI: 1996-412779/41.  
 DR N-PSDB: AAT44922.  
 XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
 PT antibody - useful for diagnosis, screening and typing, or as  
 XX immunogens  
 XX Claim 12; Page 34; 71pp; French.  
 PS Human immunodeficiency virus type 1 (HIV-1) strains are currently

CC divided into 2 major groups based on the nucleotide sequences of the  
 CC envelop gene (env): group M containing sub-groups A-G, and group O  
 CC containing the strains AN70 and WPS180. The invention relates to the  
 CC discovery of several new strains of HIV-1 which can be placed in group O,  
 CC p12env, p12env, p12env, p12env, p12env, p12env, p12env, p12env, p12env,  
 CC AN744907-19, p12env, p12env, p12env, p12env, p12env, p12env, p12env,  
 CC AN744907-19, p12env, p12env, p12env, p12env, p12env, p12env, p12env,  
 CC (MAN), 1547 (BCP08 (RNO)) and 1545 (BCF03 (RNO)). The sequence  
 CC presented here is from the strain BCF07 (MAN) and corresponds to a  
 CC fragment of the gp41 protein encoded by the env gene. The nucleic acids  
 CC can be used to detect gp. O HIV-1 strains by hybridisation or (as  
 CC strains) by gene amplification, also for screening and typing of such  
 CC to raise Ab for detecting gp. O HIV-1.  
 S0 Sequence 40 AA;  
 Query Match 91.3%; Score 115; DB 17; Length 40;  
 Best Local Similarity 86.4%; Pred. No. 3, 9e-08;  
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 LLSNGCKGRILVCYSYVQNST 22  
 Db 19 LLSNGCKGRILVCYSYVQNST 40  
 1 LLSNGCKGRILVCYSYVQNST 22  
 RESULT 6  
 ID AA80460  
 AC AA80460 standard; peptide; 22 AA.  
 XX AA80460;  
 DT 28-JUN-1999 (first entry)  
 DE Peptide derived from a conserved sequence of group O human HIV.  
 KM Group O human immune deficiency virus; HIV; detection; infection.  
 XX Synthetic.  
 XX Immune deficiency virus.  
 EN W05845323-A1.  
 PD 15-OCT-1998.  
 XX 06-APR-1998: 98MO-FR00691.  
 PR 24-FEB-1998: 98FR-0002212.  
 XX 09-APR-1997: 97FR-0004356.  
 XX (SNFI ) PASTERIS SANOFI DIAGNOSTICS SA.  
 PI Chenebaux DMB, Delagneau JFH, Gabelle SIX, Rieunier FY;  
 XX WPI, 1998-583190/49.  
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by  
 PT human immune deficiency virus of group O  
 XX Claim 6; Page 42; 55pp; French.  
 XX AA80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds) which represent variable sequences  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 S0 Sequence 22 AA;  
 Query Match 89.7%; Score 113; DB 19; Length 22;  
 Best Local Similarity 86.4%; Pred. No. 3, 9e-08;  
 Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LLSGCKGRILVCTSYVNWNT 22  
 DB 1 LLSGCKGRILVCTSYVNWNT 22

## RESULT 7

AAW07352  
 AAW07352 standard; peptide; 40 AA.

AAW07352;  
 03-JUN-1997 (first entry)

Partial sequence of gp41 from HIV-1 gp. O strain BCF13.

Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O; C23-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop; primer; hybridization; amplification; PCR; polymerase chain reaction; immunogen; antibody.

Human immunodeficiency virus type 1.

WO6627013-A1.

06-SEP-1996.

26-FEB-1996; 96NO-FR00294.

27-FEB-1995; 95FR-0002236.

(LAST-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.

(INRM) INSERM INST NAT SANTÉ & RECH MEDICALE.

Chaix-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;

WPI; 1996-412793/41.

New strains of HIV-1 group O, related DNA fragments, peptide(s) and antibodies - useful for diagnosis, screening and typing, or as immunogens

Claim 12; Page 46; 71pp; French.

Human immunodeficiency virus type 1 (HIV-1) strains are currently classified into major groups based on the nucleotide sequences of the envelope gene (env): group M containing sub-groups A-G, and group O containing the strains A1770 and WPS180. The invention relates to the discovery of several new strains of HIV-1 which can be placed in group O, based on the partial sequences of the C23-env, gp41 and gag genes (see AAT4907-39 and AAW07352-64). The novel strains have been deposited at the International Centre for Genetic Engineering and Biotechnology (ICGEB) (P.O. Box 1223, Heliopolis, Cairo, Egypt) under accession numbers IC9707 (HIV-1 group O strain A1770) and IC9708 (HIV-1 group O strain WPS180). The sequences presented here is from the strain BCF13 and corresponds to a fragment of the gp41 protein encoded by the env gene. The nucleic acids can be used to detect gp. O HIV-1 strains by hybridisation or (as primers) by gene amplification, also for screening and typing of such strains. Peptides encoded by the nucleic acids can be used as immunogens to raise Ab for detecting gp. O HIV-1.

Sequence 40 AA;

Query Match 89.7%; Score 113; DB 17; Length 40;

Best Local Similarity 86.4%; Pred. No. 7e-08;

Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSGCKGRILVCTSYVNWNT 22

DB 19 LLSGCKGRILVCTSYVNWNT 40

## RESULT 8

AAW80469

ID AAW80469 standard; peptide; 32 AA.

AAW80469;

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

WO6845323-A1.

15-OCT-1998.

06-APR-1998; 96NO-FR00691.

24-FEB-1998; 96FR-0002212.

09-APR-1997; 97FR-0004356.

(SNP) PASTEUR SMOPI DIAGNOSTICS SA.

Cheneaux DMB, Delagrange JFH, Gabelle SJX, Rieunier FY;

WPI; 1996-583190/49.

New synthetic peptide(s) - useful for e.g. detecting infection by human immune deficiency virus of group O

Claim 6; Page 44; 55pp; French.

AAW80459-74 represent synthetic peptides (either linear or cyclised by Cys-Cys disulphide bonds). The peptides represent variable regions connected around short highly conserved regions. The peptides are useful as immunological reagents for detecting infection by group O human immune deficiency virus (HIV).

Sequence 32 AA;

Query Match 88.9%; Score 112; DB 19; Length 32;

Best Local Similarity 81.8%; Pred. No. 7e-08;

Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSGCKGRILVCTSYVNWNT 22

DB 11 LLSGCKGRILVCTSYVNWNT 32

## RESULT 9

AAW07351

AAW07351 standard; peptide; 41 AA.

AAW07351;

03-JUN-1997 (first entry)

Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;

C23-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;

primer; hybridization; amplification; PCR; polymerase chain reaction;

immunogen; antibody.

Human immunodeficiency virus type 1.

WO6627013-A1.

06-SEP-1996.

26-FEB-1996; 96NO-FR00294.

XX 27-FEB-1995: 95FR-0002236.  
 PR (ASSI-) ASSISTANCE PUBLIQUE HOPITALUX PARIS.  
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX  
 PI Chaix-Baudier M., Loussert-Ajaka I., Ly T., Saragosti S., Simon F;  
 DR WPI: 1996-412779/41.  
 XX  
 PT New strains of HIV-1 group O, related DNA fragments, peptides) and  
 PT antibodies - useful for diagnosis, screening and typing, or as  
 PT immunogens  
 XX  
 CC Claim 12: Page 46; 71pp; French.  
 CC  
 CC Human immunodeficiency virus type 1 (HIV-1) strains are currently  
 CC divided into 2 major groups based on the nucleic acid sequence of the  
 CC envelope gene (env): group M containing sub-groups A, G and O, and  
 CC group O, which contains several new strains of HIV-1 which can be placed in group O,  
 CC based on the partial sequences of the C2V1-env, gp41 and gag genes (see  
 CC A19407-39 and A400339-64). The novel strains have been deposited as  
 CC (MN) 1547 (BCR08 (INO)) and (MN) 1548 (BCR07 (PANI)). The sequence  
 CC presented here is from the strain BCR12 and corresponds to the C2V1-env  
 CC of the gp41 protein encoded by the env gene. The nucleic acids can be used  
 CC to detect gp. O HIV-1 strains by hybridisation or (as primers) by gene  
 CC amplification, also for screening and typing of such strains. Peptides  
 CC encoded by the nucleic acids can be used as immunogens to raise Ab for  
 CC detecting gp. O HIV-1.  
 CC  
 SO Sequence 41 AA:  
 Query Match 88.9%; Score 112; DB 17; Length 41;  
 Best Local Similarity 81.8%; Pred. No. 9, 7e-08;  
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 1 LLSWGGKGRRLVCTYSVQNNST 22  
 DB 19 LLSWGGKGRRLVCTYSVQNNST 40  
 XX  
 XX RESULT 10  
 XX AAY05565  
 XX ID AAY05565 standard; Protein: 113 AA.  
 XX AAY05565;  
 XX  
 XX 19-JUL-1999 (first entry)  
 XX  
 XX HIV-1 group O isolate MP539-BMC gp41 antigen.  
 XX  
 XX HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;  
 XX vaccine; diagnosis; AIDS.  
 XX  
 XX Human immunodeficiency virus type 1.  
 XX  
 XX Key Location/Qualifiers  
 XX FT Misc-difference 65 /note= "encoded by AMW"  
 XX FT Misc-difference 74 /note= "encoded by ARR"  
 XX FT Misc-difference 84 /note= "encoded by GAK"  
 XX FT Misc-difference 86 /note= "encoded by AGY"  
 XX  
 XX MO9904011-A2.  
 XX  
 XX 28-JAN-1999.  
 XX  
 XX 20-JUL-1998; 98WO-EP04522.

XX 18-JUL-1997; 97EP-0870110.  
 PR (INNO-) INNOGENETICS NV.  
 XX  
 PI Delaporte E., Peeters M., Saman E., Vanden Haesevelde M;  
 DR WPI: 1999-132255/11.  
 XX  
 PT New isolated HIV-1 group O strains - used to produce  
 PT polypeptides, antigens and antibodies for use in diagnosis and in  
 PT vaccines for prevention of HIV-1 infection  
 XX  
 CC Claim 3; Fig 6; 162pp; English.  
 CC  
 CC The present sequence is an antigen of the gp41 protein of HIV-1  
 CC group O (Outlier) strain MP539-BMC, a Cameroon isolate. The  
 CC invention relates to new HIV-1 group O antigens (see AAY05546-625),  
 CC and to the use of these antigens, or nucleic acids encoding them (see  
 CC AAY25154-40), in the diagnosis, screening and typing of HIV-1 group O  
 CC used as reagents for detecting HIV-1 group O infection and for  
 CC differentiating different types of HIV-1 group O infection.  
 CC Vaccines that provide protective immunity against HIV-1 infection, in  
 CC particular against HIV-1 group O infection, comprises at least one  
 CC HIV-1 type O antigen, a nucleic acid encoding such an antigen, a  
 CC form of the antigen comprising such an antigen, or an attenuated  
 CC form of HIV-1 group O strains, mostly from patients from Cameroon and its  
 CC neighbouring countries.  
 CC  
 SO Sequence 113 AA:  
 Query Match 89.9%; Score 112; DB 20; Length 113;  
 Best Local Similarity 81.8%; Pred. No. 2, 5e-07;  
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 1 LLSWGGKGRRLVCTYSVQNNST 22  
 DB 39 LLSWGGKGRRLVCTYSVQNNST 60  
 XX  
 XX RESULT 11  
 XX AAY05625  
 XX ID AAY05625 standard; Protein: 715 AA.  
 XX AAY05625;  
 XX  
 XX 19-JUL-1999 (first entry)  
 XX  
 XX HIV-1 group O isolate MP645 envelope protein (Env).  
 XX  
 XX HIV-1 group O; Outlier strain; envelope protein; Env; antigen;  
 XX vaccine; diagnosis; AIDS.  
 XX  
 XX Human immunodeficiency virus type 1.  
 XX  
 XX MO9904011-A2.  
 XX  
 XX 28-JAN-1999.  
 XX  
 XX 20-JUL-1998; 98WO-EP04522.  
 XX  
 XX 18-JUL-1997; 97EP-0870110.  
 XX  
 XX (INNO-) INNOGENETICS NV.  
 XX  
 XX Delaporte E., Peeters M., Saman E., Vanden Haesevelde M;  
 PI WPI: 1999-132255/11.  
 DR N-PSDB; AAY25150.  
 XX  
 XX New isolated HIV-1 group O strains - used to produce

PF polynucleotides, antigens and antibodies for use in diagnosis and in  
PT vaccines for prevention of HIV-1 infection

XX Claim 3; Fig 8a, 162pp. English.

CC The present sequence is a partial Env polypeptide of HIV-1 group O  
CC (Outlier) virus isolate MP645, as deduced from part of the genome  
CC of MP645 (see AAY35180). The invention relates to new HIV-1 group O  
CC antigens, especially envelope protein antigens (see AAY05546-623),  
CC and the use of these antigens, or nucleic acids encoding them, for  
CC the diagnosis and/or prophylaxis of HIV-1 infection. They can be  
CC used as reagents for detecting HIV-1 group O infection and for  
CC differentiating different types of HIV-1 group O infection, and for  
CC vaccines that provide protective immunity against HIV-1 infection,  
CC in particular against HIV-1 group O infection, comprise at least  
CC one HIV-1 type O antigen, a nucleic acid encoding such an antigen,  
CC a virus-like particle comprising such an antigen, or an attenuated  
CC form of an HIV-1 type O strain. The antigens, nucleic acids, virus-  
CC like particles and attenuated forms are obtained from patients from Cameroon, Gabon,  
CC Tchead, Nigeria, Senegal and Niger.

XX Sequence 715 AA;

Query Match 88.9%; Score 112; DB 20; Length 715;  
Best Local Similarity 81.8%; Pred. No. 1,4e-06; 2; Indels 0; Gaps 0;  
Matches 19; Conservative 1; Mismatches 2;

OY 1 LLSWCGKGRVLCVTSVQNMST 22  
DB 628 LLSWCGKGRVLCVTSVQNMST 649

RESULT 12

XX AAB12212

XX AAB12212 standard; peptide; 33 AA.

XX AAB12212;

XX 10-NOV-2000 (first entry)

XX Partial sequence of HIV-1 strain BCF13 gp41 immunodominant region.  
XX HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;  
XX acquired immunodeficiency syndrome; group O HIV; gp41; BCF13.

XX Human immunodeficiency virus type 1.

XX EPI013766-A2.

XX 28-JUN-2000.

XX 29-NOV-1999; 99EP-0109491.

XX 30-NOV-1998; 98US-0110292.

XX 08-FEB-1999; 98US-0119138.

XX 04-NOV-1999; 99US-0433428.

XX (ORF1-4) ORF1-4 CLINICAL DIAGNOSTICS INC.

XX De Lays R, Zheng J;

XX WPI, 2000-402205/35.

XX New antigenic peptides and peptide functional derivatives, useful for  
XX detection of antibodies produced in response to human immunodeficiency  
XX virus group O antibodies -

XX Example 1; Fig 1; 52pp. English.

XX The present sequence is a partial gp41 protein of Human Immunodeficiency  
XX Virus Type 1 (HIV-1) strain BCF13. HIV is the principle aetiological  
XX agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV  
XX envelope protein, and may be used as an antigen for the detection of

CC antibodies produced in response to HIV infection. BCF13 is a member of  
CC the group O (Outlier) viruses. The present sequence is the immunodominant region  
CC of gp41. This sequence was used in a sequence homology alignment,  
CC which in turn was used to derive a consensus sequence peptide; peptide  
CC 147 (AAB12254).

XX Sequence 33 AA;

Query Match 88.1%; Score 111; DB 21; Length 33;  
Best Local Similarity 90.0%; Pred. No. 1.1e-07;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWCGKGRVLCVTSVQNM 20  
DB 14 LLSWCGKGRVLCVTSVQNM 33

RESULT 13

XX AAY05559

XX AAY05559 standard; Protein; 113 AA.

XX AAY05559;

XX 19-JUL-1999 (first entry)

XX HIV-1 group O isolate BSD189 gp41 antigen.

XX HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;  
XX vaccine; diagnosis; AIDS.

XX Human immunodeficiency virus type 1.

XX WO9904011-A2.

XX 28-JAN-1999.

XX 20-JUL-1996; 98WO-EP04522.

XX 18-JUL-1997; 97EP-0870110.

XX (IRNO-) INNOCENTICS NV.

XX Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;

XX WPI, 1999-112255/11.

XX N-PSDB; AAY25167.

XX New isolated HIV-1 group O strains - used to produce  
XX PT polynucleotides, antigens and antibodies for use in diagnosis and in  
XX vaccines for prevention of HIV-1 infection

XX Claim 3; Fig 6; 162pp. English.

XX The present sequence is an antigen of the gp41 protein of HIV-1  
XX group O (Outlier) strain BSD189, a Cameroon isolate. The  
XX invention relates to new HIV-1 group O antigens (see AAY05546-623),  
XX and the use of these antigens, or nucleic acids encoding them (see  
XX AAY23154-80), in the diagnosis and prophylaxis of HIV-1 infection.  
XX They can be used as reagents for detecting HIV-1 group O infection and for  
XX differentiating different types of HIV-1 group O infection, and for  
XX vaccines that provide protective immunity against HIV-1 infection,  
XX in particular against HIV-1 group O infection, comprise at least one  
XX HIV-1 type O antigen, a nucleic acid encoding such an antigen, a  
XX virus-like particle comprising such an antigen, or an attenuated  
XX form of an HIV-1 type O strain. The invention also relates to new  
XX HIV-1 group O strains, mostly from patients from Cameroon and its  
XX neighbouring countries.

XX Sequence 113 AA;

Query Match 88.1%; Score 111; DB 20; Length 113;  
Best Local Similarity 81.8%; Pred. No. 3.3e-07;  
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

XX 1 LLSWCKGRIVCTYSVQNMST 22  
 XX 1 LLSWCKGRIVCTYSVQNMST 22  
 DB 39 LLSWCKGRIVCTYSVQNMST 50

RESULT 14  
 AAM1231 standard; peptide: 33 AA.  
 AAM1231;  
 10-NOV-2000 (first entry)

Partial sequence of HIV-1 strain MAN gp41 immunodominant region.  
 HIV-1, AIDS, human immunodeficiency virus type 1; immunodominant region;  
 acquired immunodeficiency syndrome; group O HIV; gp41; MAN.  
 Human immunodeficiency virus type 1.  
 EPI013766-A2.  
 28-JUN-2000.  
 29-NOV-1999; 99EP-0309491.  
 30-NOV-1998; 98US-0110292.  
 08-FEB-1999; 99US-0119138.  
 04-NOV-1999; 99US-0433428.  
 (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.  
 De Lays R, Zheng J;  
 WPI: 2000-402205/35.  
 New antigenic peptides and peptide functional derivatives, useful for  
 detecting antibodies produced in response to human immunodeficiency  
 virus group O antibodies -  
 Example 1; Fig 1; 52pp; English.  
 The present sequence is a partial gp41 protein of Human immunodeficiency  
 virus type 1 (HIV-1) strain MAN. HIV is the principle aetiological  
 agent of acquired immunodeficiency syndrome (AIDS). gp41 is a HIV  
 envelope protein and is the major target for the detection of  
 antibodies produced in response to HIV infection for the immunodominant  
 HIV group O (outlier). The present sequence is the immunodominant region  
 of gp41. This sequence was used in a sequence homology alignment, peptide  
 which in turn was used to derive a consensus sequence peptide: peptide  
 147 (AAM1234).

Sequence 33 AA;  
 Query Match 87.3%; Score 110; DB 21; Length 33;  
 Best Local Similarity 90.0%; Pred. No. 1.4e-07;  
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 1 LLSWCKGRIVCTYSVQNM 20  
 14 LLSWCKGRIVCTYSVQNM 33

RESULT 15  
 AAM07343 standard; peptide: 40 AA.  
 AAM07343;  
 03-JUN-1997 (first entry)  
 Partial sequence of gp41 from HIV-1 gp. O strain BCF02 (ESS).

XX Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;  
 XX C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;  
 XX primer; hybridization; amplification; PCR; polymerase chain reaction;  
 XX immunogen; antibody.  
 XX Human immunodeficiency virus type 1.  
 XX W0962703-A1.  
 XX 06-SEP-1996.  
 XX 26-FEB-1996; 96MO-FR00294.  
 XX 27-FEB-1995; 95FR-0002226.  
 XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX Chail-Baudier M., Lousset-Ajaka I., Ly T., Saragosti S., Simon F.  
 XX WPI: 1996-412779/41.  
 XX N-ESDB: AAT44918.  
 XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
 XX antibodies - useful for diagnosis, screening and typing, or as  
 XX immunogens  
 XX Claim 12; Page 33; 71pp; French.  
 XX Human immunodeficiency virus type 1 (HIV-1) strains are currently  
 XX divided into 2 major groups based on the nucleotide sequences of the  
 XX envelope gene (env): group M containing sub-groups A-G, and group O  
 XX containing the strains ANR70 and WPS180. The invention relates to the  
 XX discovery of several new strains of HIV-1 which can be placed in group O,  
 XX based on the sequence of the gp41 gene. The invention also relates to  
 XX AAT44907-39 and AAM07323-64). The novel 12-mer gp41 and gag genes (see  
 XX (MAN)), 1547 (BCP08 (NKO)) and 1545 (BCP03 (PCO)). The sequence  
 XX presented here is from the strain BCF02 (ESS) and corresponds to a  
 XX fragment of the gp41 protein encoded by the env gene. The nucleic acids  
 XX primer used to detect gp. O HIV-1 strains by hybridization or (as  
 XX primers). Peptides encoded by the nucleic acids can be used as immunogens  
 XX to raise Ab for detecting gp. O HIV-1.

Sequence 40 AA;  
 Query Match 87.3%; Score 110; DB 17; Length 40;  
 Best Local Similarity 91.8%; Pred. No. 1.7e-07;  
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 1 LLSWCKGRIVCTYSVQNMST 22  
 19 LLSWCKGRIVCTYSVQNMST 40

Search completed: May 29, 2003, 10:36:21  
 Job time : 29.333 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:36 Search time 9,95238 Seconds

(Without alignments)  
65,040 Million cell updates/sec

Title: US-09-147-362A-4

Perfect score: 126

Sequence: 1 LLSMGKGRALVCYVQNMST 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 2942292 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing filter 45 summaries

Database: Issued Patents, AA:  
1: /cgn2\_6/pdata/1/1aa/5A.COMB.pap.\*  
2: /cgn2\_6/pdata/1/1aa/5B.COMB.pap.\*  
3: /cgn2\_6/pdata/1/1aa/6A.COMB.pap.\*  
4: /cgn2\_6/pdata/1/1aa/6B.COMB.pap.\*  
5: /cgn2\_6/pdata/1/1aa/PTTUS.COMB.pap.\*  
6: /cgn2\_6/pdata/1/1aa/backfile1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	91.3	40	3	US-08-894-699-39, Appl
2	115	91.3	40	3	US-08-894-699-39, Appl
3	115	91.3	40	3	US-08-894-699-39, Appl
4	113	88.7	40	4	US-09-444-410-42, Appl
5	113	88.7	40	4	US-09-444-410-42, Appl
6	112	88.9	41	3	US-08-894-699-67, Appl
7	112	88.9	41	3	US-08-894-699-67, Appl
8	111	88.1	43	4	US-09-433-428D-6, Appl
9	111	88.1	43	4	US-09-433-428D-6, Appl
10	110	87.3	40	3	US-08-894-699-36, Appl
11	110	87.3	40	3	US-08-894-699-36, Appl
12	110	87.3	40	4	US-09-444-410-37, Appl
13	110	87.3	41	3	US-08-894-699-69, Appl
14	110	87.3	41	3	US-08-894-699-69, Appl
15	108	85.7	37	4	US-09-433-428D-15, Appl
16	108	85.7	37	4	US-09-433-428D-15, Appl
17	108	85.7	37	4	US-09-433-428D-15, Appl
18	108	85.7	40	4	US-09-444-410-37, Appl
19	108	85.7	40	4	US-09-444-410-37, Appl
20	108	85.7	215	2	US-08-912-129A-58, Appl
21	108	85.7	215	2	US-08-912-129A-58, Appl
22	108	85.7	373	2	US-08-912-129A-52, Appl
23	108	85.7	460	2	US-08-912-129A-60, Appl
24	108	85.7	438	2	US-08-912-129A-50, Appl
25	108	85.7	438	2	US-08-912-129A-50, Appl
26	108	85.7	873	2	US-08-912-129A-64, Appl
27	107	84.9	33	4	US-09-433-428D-8, Appl

28	107	84.9	40	3	US-08-894-699-40, Appl
29	107	84.9	40	3	US-08-894-699-40, Appl
30	105	83.3	40	3	US-08-894-699-42, Appl
31	105	83.3	40	3	US-08-894-699-42, Appl
32	105	83.3	40	3	US-08-894-699-42, Appl
33	105	83.3	356	4	US-08-986-453-12, Appl
34	104	82.5	23	4	US-09-433-428D-68, Appl
35	104	82.5	33	4	US-09-433-428D-4, Appl
36	104	82.5	33	4	US-09-433-428D-4, Appl
37	104	82.5	33	4	US-09-433-428D-7, Appl
38	104	82.5	33	4	US-09-433-428D-15, Appl
39	104	82.5	33	4	US-09-433-428D-15, Appl
40	104	82.5	42	4	US-08-894-699-66, Appl
41	103	81.7	33	4	US-09-433-428D-5, Appl
42	103	81.7	33	4	US-09-433-428D-14, Appl
43	103	81.7	33	4	US-09-433-428D-29, Appl
44	102	81.0	33	4	US-09-433-428D-10, Appl
45	102	81.0	33	4	US-09-433-428D-18, Appl

## ALIGNMENTS

RESULT 1  
US-08-894-699-39  
Sequence 39, Application US/08894699  
Priority: 08-06-1996  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSCI, SEPTOB  
APPLICANT: LOUSSERT-ALAKI, IBITISSAM  
APPLICANT: LY, THOI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUPE HIV-1, FRAGMENTES OF SUCH  
TITLE OF INVENTION: GROUPE HIV-1, FRAGMENTES OF SUCH  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OELON, SPIVAK, MCCELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
FLOOR  
STATE: ARIZONA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION RELEASE #1.0, Version #1.30  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION: FR 95/02236  
APPLICATION NUMBER: 95-02236  
ATTORNEY/AGENT INFORMATION:  
NAME: OELON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REGISTRATION/DOCKET NUMBER: 0354-0020-0PCT  
TELEPHONE: 703-413-1000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
FEATURES: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-08-894-699-39  
Query Match 91.3%, Score 115; DB 3; Length 40;  
Best Local Similarity 86.4%; Pred. No. 5e-10;  
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
OY 1 LLSGCKGRKLVCTSYVMNET 22  
DB 19 LLSGCKGRKLVCTSYVMNET 40  
RESULT 2  
US-09-444-410-39  
Sequence 39, Application US/09444410  
Patent No. 627093769  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARACOSTI, SEXTON  
APPLICANT: LOUSBERT-ALAKA, IBTITSSAM  
APPLICANT: LY, THOI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
SOFTWARE: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA: Patent in Release #1.0, Version #1.30  
APPLICATION NUMBER: US/09444.410  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
FILING DATE NUMBER: 08/894.699  
FILING DATE: 27-FEB-1995  
APPLICATION NUMBER: PR 95/02236  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-OPCT  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STANDARDS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-444-410-39  
Query Match 91.3%, Score 115; DB 4; Length 40;  
Best Local Similarity 86.4%; Pred. No. 5e-10; 1; Indels 0; Gaps 0;  
Matches 19; Conservative 2; Mismatches 0; Gaps 0;  
OY 1 LLSGCKGRKLVCTSYVMNET 22  
DB 19 LLSGCKGRKLVCTSYVMNET 40

RESULT 3  
US-08-894-699-68  
Sequence 68, Application US/08894699  
Patent No. 6030769  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARACOSTI, SEXTON  
APPLICANT: LOUSBERT-ALAKA, IBTITSSAM  
APPLICANT: LY, THOI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: Patent in Release #1.0, Version #1.30  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
FILING DATE NUMBER: PR 95/02236  
FILING DATE: 27-FEB-1995  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-OPCT  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STANDARDS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-68  
Query Match 89.7%, Score 113; DB 3; Length 40;  
Best Local Similarity 86.4%; Pred. No. 9.7e-10;  
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
OY 1 LLSGCKGRKLVCTSYVMNET 22  
DB 19 LLSGCKGRKLVCTSYVMNET 40  
RESULT 4  
US-09-444-410-68  
Sequence 68, Application US/09444410  
Patent No. 627093769  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARACOSTI, SEXTON  
APPLICANT: LOUSBERT-ALAKA, IBTITSSAM  
APPLICANT: LY, THOI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE



TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: P.C.  
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 STATE: ARLINGTON  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/444,410  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/894,699  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 68:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 40 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-894-410-68

Query Match 89.7%; Score 113; DB 4; Length 40;  
 Best Local Similarity 86.4%; Pred. No. 9.7e-10;  
 Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 LLSWCGCKRGLVCTSYVKNST 22  
 19 LLSWCGCKRGLVCTSYVKNST 40

RESULT 5  
 US-08-894-699-67  
 Sequence 67 Application US/08894699  
 Patent No. 6270975  
 GENERAL INFORMATION:  
 APPLICANT: SIMON, FRANCOIS  
 APPLICANT: SARAGOSTI, SEYTOB  
 APPLICANT: LOUSBERT-AJAKA, IBITISSAM  
 APPLICANT: CHAI-BANDIER, MARIE-LAURE  
 APPLICANT: LY, THOM-DIONG  
 TITLE OF INVENTION: HIV-1, FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: P.C.  
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA

ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/894,699  
 FILING DATE: 01-DEC-1997  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/FR96/00294  
 FILING DATE: 26-FEB-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 67:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 41 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-894-699-67

Query Match 88.9%; Score 112; DB 3; Length 41;  
 Best Local Similarity 81.8%; Pred. No. 1.4e-09;  
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 LLSWCGCKRGLVCTSYVKNST 22  
 19 LLSWCGCKRGLVCTSYVKNST 40

RESULT 6  
 US-09-444-410-67  
 Sequence 67 Application US/99444410  
 Patent No. 6270975  
 GENERAL INFORMATION:  
 APPLICANT: SIMON, FRANCOIS  
 APPLICANT: SARAGOSTI, SEYTOB  
 APPLICANT: LOUSBERT-AJAKA, IBITISSAM  
 APPLICANT: CHAI-BANDIER, MARIE-LAURE  
 APPLICANT: LY, THOM-DIONG  
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: P.C.  
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/444,410  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:

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      APPLICATION NUMBER: 08/894,699
      FILING DATE: 27-FEB-1995
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: FR 95/02236
      FILING DATE: 27-FEB-1995
      ATTORNEY/AGENT INFORMATION:
      NAME: OBLON, NORMAN F., 614
      RESERVATION NUMBER: 0354-0020-0PCT
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 703-413-3000
      TELEFAX: 703-413-2220
      INFORMATION FOR SEQ ID NO: 67:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 41 amino acids
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
      09-443-410-67

Query Match 88.94; Score 112; DB 4; Length 41;
      Similarity 88.94; Pct. 2.1e-09;
      Best Local 90.08; Mismatches 1; Indels 0; Gaps 0;
      Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

      1 LLSWGCKGRIVCYTSYVNMST 22
      19 LLSWGCKGRIVCYTSYVNMST 40
      DB

RESULT 7
US-09-433-428D-6
      Sequence 6, Application US/09433428D
      Patent No. 6149910
      GENERAL INFORMATION:
      APPLICANT: De Lays, Robert J.
      APPLICANT: Zheng, Jian
      TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
      FILE REFERENCE: IDS-202
      CURRENT APPLICATION NUMBER: US/09/433,428D
      CURRENT FILING DATE: 1999-11-04
      NUMBER OF SEQ ID NOS: 70
      SOFTWARE: Patentin Ver. 2.0
      SEQ ID NO 6
      TYPE: PRT
      ORGANISM: Human immunodeficiency virus type 1
      09-433-428D-6

Query Match 88.14; Score 111; DB 4; Length 33;
      Similarity 88.14; Pct. 1.5e-09;
      Best Local 90.08; Mismatches 2; Indels 0; Gaps 0;
      Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

      1 LLSWGCKGRIVCYTSYVNM 20
      14 LLSWGCKGRIVCYTSYVNM 33
      DB

RESULT 8
US-09-433-428D-35
      Sequence 25, Application US/09433428D
      Patent No. 6149910
      GENERAL INFORMATION:
      APPLICANT: De Lays, Robert J.
      APPLICANT: Zheng, Jian
      TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
      FILE REFERENCE: IDS-202
      CURRENT APPLICATION NUMBER: US/09/433,428D
      CURRENT FILING DATE: 1999-11-04
      NUMBER OF SEQ ID NOS: 70
      SOFTWARE: Patentin Ver. 2.0
      SEQ ID NO 25
      LENGTH: 33

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      TYPE: PRT
      ORGANISM: Human immunodeficiency virus type 1
      09-433-428D-25

Query Match 87.34; Score 110; DB 4; Length 33;
      Similarity 87.34; Pct. 2.1e-09;
      Best Local 90.08; Mismatches 2; Indels 0; Gaps 0;
      Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

      1 LLSWGCKGRIVCYTSYVNM 20
      14 LLSWGCKGRIVCYTSYVNM 33
      DB

RESULT 9
US-08-894-699-36
      Sequence 3, Application US/08894699
      Patent No. 6030769
      GENERAL INFORMATION:
      APPLICANT: SIMON, FRANCOIS
      APPLICANT: SARAGOSTI, SENTOB
      APPLICANT: LOUSBERT-AJAKA, IBITISSAM
      APPLICANT: LY, THOM-DONG
      TITLE OF INVENTION: GROUP O HIV-1 FRAGMENTS OF SUCH
      TITLE OF INVENTION: VIRUSES, AND USES THEREOF
      NUMBER OF SEQUENCES: 81
      CORRESPONDENCE ADDRESS:
      ADDRESSER: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
      STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
      CITY: ARLINGTON
      STATE: VA
      COUNTRY: USA
      ZIP: 22202
      COMPUTER READABLE FORM:
      MEDIUM TYPE: floppy disk
      OPERATING SYSTEM: PC DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/894,699
      FILING DATE: 01-DEC-1997
      CLASSIFICATION: DNA:
      PRIOR APPLICATION NUMBER: PCT/FR96/00294
      FILING DATE: 26-FEB-1996
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: FR 95/02236
      FILING DATE: 27-FEB-1995
      ATTORNEY/AGENT INFORMATION:
      NAME: OBLON, NORMAN F., 614
      RESERVATION NUMBER: 0354-0020-0PCT
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 703-413-3000
      TELEFAX: 703-413-2220
      INFORMATION FOR SEQ ID NO: 36:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 41 amino acids
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
      08-894-699-36

Query Match 87.34; Score 110; DB 3; Length 40;
      Similarity 87.34; Pct. 2.6e-09;
      Best Local 90.08; Mismatches 1; Indels 0; Gaps 0;
      Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

      1 LLSWGCKGRIVCYTSYVNMST 22
      19 LLSWGCKGRIVCYTSYVNMST 40
      DB

```

RESULT 10  
 US-08-894-699-37  
 Sequence 37, Application US/08894699  
 Patent No. 6030769  
 GENERAL INFORMATION:  
 APPLICANT: SIMON, FRANCOIS  
 APPLICANT: LOUISBERT-ALIXA, IBITISSAM  
 APPLICANT: LY, THOI-DUONG  
 APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: P.C.  
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/894,699  
 FILING DATE: 27-FEB-1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/FR96/00294  
 FILING DATE: 26-FEB-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 NAME: OHLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3400  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 37:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 40  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-894-699-37

Query Match  
 Best local Similarity 81.3%; 2 e-09;  
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 LLSMCGKGRILCVTSYVNKST 22  
 19 LLSMCGKGRILCVTSYVNKST 40

RESULT 11  
 US-09-444-410-36  
 Sequence 36, Application US/09444410  
 Patent No. 6270975  
 GENERAL INFORMATION:  
 APPLICANT: SIMON, FRANCOIS  
 APPLICANT: LOUISBERT-ALIXA, IBITISSAM  
 APPLICANT: LY, THOI-DUONG  
 APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: P.C.  
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/444,410  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/894,699  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OHLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3400  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 40  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-444-410-36

APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: P.C.  
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/444,410  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/894,699  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OHLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3400  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 40  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-444-410-36

Query Match  
 Best local Similarity 81.8%; Pred. No. 2.6e-09;  
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 LLSMCGKGRILCVTSYVNKST 22  
 19 LLSMCGKGRILCVTSYVNKST 40

RESULT 12  
 US-09-444-410-37  
 Sequence 37, Application US/09444410  
 Patent No. 6270975  
 GENERAL INFORMATION:  
 APPLICANT: SIMON, FRANCOIS  
 APPLICANT: LOUISBERT-ALIXA, IBITISSAM  
 APPLICANT: LY, THOI-DUONG  
 APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: P.C.  
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/444,410  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/894,699  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OHLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3400  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 40  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-444-410-36

COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/444,410  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/894,699  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 37:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 40 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-444-410-37

Query Match 87.3% Score 110; DB 4; Length 40;  
 Best Local Similarity 81.8%; Pred. No. 2.6e-09;  
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 LLSMCKGRVCYTSVNMNST 22  
 Db 19 LNTMCKGRVCYTSVNMNST 40

RESULT 13  
 US-09-444-410-69  
 Sequence 69, Application US/08894699  
 Patent No. 6030769  
 GENERAL INFORMATION:  
 APPLICANT: SIMON, FRANCOIS  
 APPLICANT: SARAGOSTI, SEBASTIEN  
 APPLICANT: LOUSSERT-ALAKA, IBITISSAM  
 APPLICANT: LY, THOI-DUONG MARIE-LAURE  
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ADDRESS: P.C.  
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 STREET, FLOOR  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/894,699  
 FILING DATE: 01-DEC-1997  
 CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/FR96/00294  
 FILING DATE: 26-FEB-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 69:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 41 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-894-699-69

Query Match 87.3% Score 110; DB 3; Length 41;  
 Best Local Similarity 81.8%; Pred. No. 2.7e-09;  
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 LLSMCKGRVCYTSVNMNST 22  
 Db 19 LNTMCKGRVCYTSVNMNST 40

RESULT 14  
 US-09-444-410-69  
 Sequence 69, Application US/09444410  
 Patent No. 6270975  
 GENERAL INFORMATION:  
 APPLICANT: SIMON, FRANCOIS  
 APPLICANT: SARAGOSTI, SEBASTIEN  
 APPLICANT: LOUSSERT-ALAKA, IBITISSAM  
 APPLICANT: LY, THOI-DUONG MARIE-LAURE  
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ADDRESS: P.C.  
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 STREET, FLOOR  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/444,410  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/894,699  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000  
 FAX: 703-413-2220  
 INVENTOR: ROBERT J. ROBERTS  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 41 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-444-410-63

Query Match 87.3%; Score 110; DB 4; Length 41;  
 Best Local Similarity 81.8%; Pred. No. 2,7e-09;  
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTSVQWNST 22  
 DB 19 LLSWGCKGRIVCYTSVQWNST 40

US-09-433-428D-30  
 Sequence 30; Application US/09433428D  
 Patent No. 6149910  
 GENERAL INFORMATION:  
 INVENTOR: ROBERT J. ROBERTS  
 APPLICANT: Zhenyi Biotech, Inc.  
 TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
 FILE REFERENCE: CDS-207  
 CURRENT APPLICATION NUMBER: US/09/433,428D  
 CURRENT FILING DATE: 1999-11-04  
 NUMBER OF SEQ ID NOS: 70  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO: 30  
 LENGTH: 33  
 TYPE: PRT  
 ORGANISM: Human immunodeficiency virus type 1  
 US-09-433-428D-30

Query Match 85.7%; Score 108; DB 4; Length 33;  
 Best Local Similarity 85.0%; Pred. No. 4.2e-09;  
 Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCKGRIVCYTSVQW 20  
 DB 14 LLSWGCKGRIVCYTSVQW 33

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 time: 9.95238 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:39:21, Search time 19.0317 Seconds

(without alignments)  
117.011 Million cell updates/sec

Title: US-09-147-362a-4

Sequence: 1 LLSWNGKRLVCTYSVQNMSTR 22

Scoring table: BLOSUM62

Gap: 10.0, Gapext: 0.5

Searched: 383519 seqs, 101232694 residues

1 number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Layering filter 45 summaries

Database:

Published Applications AA:  
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2: /cgn2\_6/prodata/2/pubpaa/PC75\_NEM\_PUB pep.\*  
3: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB pep.\*  
4: /cgn2\_6/prodata/2/pubpaa/US07\_NEM\_PUB pep.\*  
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8: /cgn2\_6/prodata/2/pubpaa/US08\_NEM\_PUB pep.\*  
9: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB pep.\*  
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11: /cgn2\_6/prodata/2/pubpaa/US10\_PUBCOMB pep.\*  
12: /cgn2\_6/prodata/2/pubpaa/US60\_NEM\_PUB pep.\*  
13: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB pep.\*  
14: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a greater score than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	108	85.7	200	10	US-09-147-362a-4
2	108	85.7	200	10	US-09-147-362a-4
3	108	85.7	245	1	US-08-911-824-56
4	108	85.7	245	1	US-08-911-824-56
5	108	85.7	281	1	US-08-911-824-120
6	108	85.7	373	1	US-08-911-824-52
7	108	85.7	460	1	US-08-911-824-50
8	108	85.7	468	1	US-08-911-824-95
9	108	85.7	526	1	US-08-911-824-97
10	108	85.7	618	1	US-08-911-824-54
11	108	85.7	706	1	US-08-911-824-93
12	108	85.7	776	1	US-08-911-824-91
13	108	85.7	873	1	US-08-911-824-61
14	108	85.7	873	1	US-08-911-824-61
15	108	85.7	873	1	US-08-911-824-61
16	108	85.7	873	1	US-08-911-824-61
17	108	85.7	873	1	US-08-911-824-61
18	108	85.7	873	1	US-08-911-824-61
19	108	85.7	873	1	US-08-911-824-61
20	108	85.7	873	1	US-08-911-824-61

20	101	80.2	37	9	US-10-026-741-94	Sequence 94, Appl
21	101	80.2	104	9	US-10-026-741-100	Sequence 100, Appl
22	100	79.4	37	9	US-10-026-741-88	Sequence 88, Appl
23	100	79.4	213	5	US-09-884-816-103	Sequence 103, Appl
24	98	77.8	35	9	US-09-886-150-62	Sequence 62, Appl
25	98	77.8	35	9	US-09-886-149-62	Sequence 62, Appl
26	98	77.8	35	9	US-09-886-159-62	Sequence 62, Appl
27	98	77.8	146	12	US-10-000-321-105	Sequence 105, Appl
28	98	77.8	204	9	US-09-884-816-105	Sequence 105, Appl
29	98	77.8	351	9	US-09-886-150-46	Sequence 46, Appl
30	98	77.8	351	9	US-09-886-149-46	Sequence 46, Appl
31	98	77.8	351	9	US-09-886-159-46	Sequence 46, Appl
32	98	77.8	351	9	US-09-886-159-46	Sequence 46, Appl
33	98	77.8	351	9	US-09-886-159-46	Sequence 46, Appl
34	97	77.0	23	9	US-09-388-847-40	Sequence 40, Appl
35	96	76.2	23	9	US-10-000-321-102	Sequence 102, Appl
36	96	76.2	23	12	US-10-000-321-102	Sequence 102, Appl
37	96	76.2	23	9	US-10-026-741-94	Sequence 94, Appl
38	96	76.2	139	9	US-09-884-816-81	Sequence 81, Appl
39	96	76.2	139	9	US-10-026-741-84	Sequence 84, Appl
40	95	67.5	37	9	US-10-026-741-84	Sequence 84, Appl
41	85	67.5	198	10	US-09-884-816-77	Sequence 77, Appl
42	85	67.5	198	10	US-09-884-816-78	Sequence 78, Appl
43	85	67.5	198	10	US-09-884-816-80	Sequence 80, Appl
44	85	67.5	198	10	US-09-884-816-83	Sequence 83, Appl
45	85	67.5	204	10	US-09-884-816-83	Sequence 106, Appl

## ALIGNMENTS

RESULT 1  
US-10-026-741-94  
Publication No. US2001004960A1  
GENERAL INFORMATION:

APPLICANT: CHAREAU, PIERRE

CLAVEL, FRANCOISE

BORIAN, ANDREW

QUILLIENT, CAROLINE

GUERIN, DENISE

NOTRE-DAMIE

DONON DE SAINT-MARTIN, JACQUELINE

COHEN, JACQUES

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE 1OR

SURVEYED ANTIGENS

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSES: Rimegan, Henderson, Fairbow, Garrett &

STREET: 1100 I Street, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/026-741

FILING DATE: 27-Dec-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/817,441

FILING DATE: 31-Aug-1998

APPLICATION NUMBER: PCT/FR 95/01391

FILING DATE: 20-Oct-1995

APPLICATION NUMBER: FR 9412554

FILING DATE: 20-Oct-1994

APPLICATION NUMBER: FR 950526

FILING DATE: 1995

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.  
 REFERENCE/DOCKET NUMBER: 03260.6005-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 86:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 86:  
 US-10-026-741-86

Query Match 85.7%; Score 108; DB 9; Length 37;  
 Best Local Similarity 81.8%; Pseq No. 1,2e-08;  
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTSVQVNST 22  
 DB 14 LLSWGCKGRIVCYTSVQVNST 35

RESULT 2  
 US-09-854-816-104  
 Sequence 104, Application US/09854816  
 Patent No. US20020151473A1  
 GENERAL INFORMATION:  
 APPLICANT: Andrew C. Barabsted  
 J. Christopher Phelan  
 Robert S. McDowell  
 Melissa A. Starovanshik  
 James A. Wells  
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
 NUMBER OF SEQUENCES: Making Same  
 CORRESPONDENCE ADDRESS:  
 ADDRESSES: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94025  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA: US/09/854, 816  
 FILING DATE: 03/01/2001  
 CLASSIFICATION: <UNKNOWN>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/965,056  
 FILING DATE: <UNKNOWN>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Forchla, R.H., Timothy E.  
 ADDRESS: 3000 University Ave.  
 TELECOMMUNICATION INFORMATION: P1005R2  
 TELEPHONE: 650/225-8674  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 104:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 200 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 104:

Query Match 85.7%; Score 108; DB 10; Length 200;  
 Best Local Similarity 81.8%; Pseq No. 5.9e-08;  
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTSVQVNST 22  
 DB 126 LLSWGCKGRIVCYTSVQVNST 147

RESULT 3  
 US-08-911-824-48  
 Sequence 58, Application US/08911824  
 Publication No. US20030004223A1  
 GENERAL INFORMATION:  
 APPLICANT: Abbott Laboratories  
 APPLICANT: Abbott Laboratories, Jr.  
 APPLICANT: Yamanishi, Julie  
 APPLICANT: Goldman, Alan M.  
 APPLICANT: Brennan, Catherine A.  
 APPLICANT: Hickman, Robert K.  
 APPLICANT: Devare, Sushil G.  
 TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
 TITLE REFERENCE: US 01  
 CURRENT APPLICATION NUMBER: US/08/911, 824  
 CURRENT FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 121  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 58  
 LENGTH: 215  
 TYPE: amino acid  
 ORGANISM: Human Immunodeficiency Virus  
 FEATURE:  
 OTHER INFORMATION: Encodes recombinant protein pCO-8PL  
 US-08-911-824-58

Query Match 85.7%; Score 108; DB 1; Length 215;  
 Best Local Similarity 87.3%; Pseq No. 6e-08;  
 Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 LLSWGCKGRIVCYTSVQVNST 22  
 DB 127 LLSWGCKGRIVCYTSVQVNST 148

RESULT 4  
 US-08-911-824-48  
 Sequence 48, Application US/08911824  
 Publication No. US20030004223A1  
 GENERAL INFORMATION:  
 APPLICANT: Abbott Laboratories  
 APPLICANT: Abbott Laboratories, Jr.  
 APPLICANT: Yamanishi, Julie  
 APPLICANT: Goldman, Alan M.  
 APPLICANT: Brennan, Catherine A.  
 APPLICANT: Hickman, Robert K.  
 APPLICANT: Devare, Sushil G.  
 TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
 TITLE REFERENCE: US 01  
 CURRENT APPLICATION NUMBER: US/08/911, 824  
 CURRENT FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 121  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 48  
 LENGTH: 245  
 TYPE: amino acid  
 ORGANISM: Human Immunodeficiency Virus  
 FEATURE:  
 OTHER INFORMATION: Encodes recombinant protein pCO-9PL  
 US-08-911-824-48

Query Match 85.7%; Score 108; DB 1; Length 245;





QY 1 LLSWGCKGRGLVCTSVQNMST 22  
DB 127 LNLWGCKGRGLVCTSVQNMST 148

RESULT 9  
US-08-911-824-50  
Sequence 50, Application US/08911824  
Publication No. US2003004323A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Golden, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Devare, Sushil G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165.US.01  
CURRENT FILING DATE: 1997-08-15  
CURRENT APPLICATION NUMBER: US/08/911.824  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 50  
LENGTH: 490  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: Encodes recombinant protein pCO-9CKS  
US-08-911-824-50

Query Match 85.7%; Score 108; DB 1; Length 490;  
Best Local Similarity 77.3%; Pred. No. 1.4e-07;  
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 LLSWGCKGRGLVCTSVQNMST 22  
DB 372 LNLWGCKGRGLVCTSVQNMST 393

RESULT 10  
US-08-911-824-97  
Sequence 97, Application US/08911824  
Publication No. US2003004323A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Golden, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Devare, Sushil G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165.US.01  
CURRENT FILING DATE: 1997-08-15  
CURRENT APPLICATION NUMBER: US/08/911.824  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 97  
LENGTH: 526  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: Encodes recombinant protein pCO-15CKS  
US-08-911-824-97

Query Match 85.7%; Score 108; DB 1; Length 526;  
Best Local Similarity 77.3%; Pred. No. 1.5e-07;  
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCKGRGLVCTSVQNMST 22  
DB 372 LNLWGCKGRGLVCTSVQNMST 393

RESULT 11  
US-08-911-824-54  
Sequence 54, Application US/08911824  
Publication No. US2003004323A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Yamaguchi, Julie  
APPLICANT: Golden, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Devare, Sushil G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165.US.01  
CURRENT FILING DATE: 1997-08-15  
CURRENT APPLICATION NUMBER: US/08/911.824  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 54  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: Encodes recombinant protein pCO-11CKS  
US-08-911-824-54

Query Match 85.7%; Score 108; DB 1; Length 618;  
Best Local Similarity 77.3%; Pred. No. 1.7e-07;  
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 LLSWGCKGRGLVCTSVQNMST 22  
DB 372 LNLWGCKGRGLVCTSVQNMST 393

RESULT 12  
US-08-911-824-93  
Sequence 93, Application US/08911824  
Publication No. US2003004323A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Yamaguchi, Julie  
APPLICANT: Golden, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Devare, Sushil G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165.US.01  
CURRENT FILING DATE: 1997-08-15  
CURRENT APPLICATION NUMBER: US/08/911.824  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 93  
LENGTH: 706  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: Encodes recombinant protein pCO-13CKS  
US-08-911-824-93

Query Match 85.7%; Score 108; DB 1; Length 706;  
Best Local Similarity 77.3%; Pred. No. 1.9e-07;  
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 LLSWGCKGRGLVCTSVQNMST 22

Db 618 LNLWGCKGRLLCYTSVKWNET 639

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RESULT 13
US-08-911-824-91
Sequence 911 Application US/08911824
US-08-911-824-91 US/08911824
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Naife
APPLICANT: Golden, Alan M.
APPLICANT: Hackett, John R., Jr.
APPLICANT: Hickman, Robert X.
APPLICANT: Deware, Stethli G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
TREATMENT OF HIV INFECTION
PRIORITY REFERENCE: AT 06/501,001 US/06/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 91
SEQ ID NO 92
SEQ ID NO 93
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-12CKS
US-08-911-824-91

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RESULT 14
US-08-911-824-61
Sequence 61 Application US/08911824
GENERAL INFORMATION
  SEQ ID NOS: 100094323A1
  APPLICANT: Abbott Laboratories
  APPLICANT: Hackett, John R., Jr.
  APPLICANT: Yamaguchi, Julie
  APPLICANT: Golden, Alan M.
  APPLICANT: Berman, Catherine A.
  APPLICANT: Berman, Catherine A.
  APPLICANT: Dewate, Shelli K.
  TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
  TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
  FILE REFERENCE: 6165 US 01
  CURRENT APPLICATION NUMBER: US/08/911,824
  PRIORITY REFERENCE: 08-08-13
  NUMBER OF SEQ ID NOS: 121
  SOFTWARE: PatSeqO For Windows Version 3.0
  SEQ ID NO: 61
  LENGTH: 873
  TYPE: PRT
  ORIGIN: Human Immunodeficiency Virus
  FEATURE:
  OTHER INFORMATION: HIV-1 Group O isolate HAM12
US-08-911-824-61 Group O isolate HAM12

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Db 601 LNLWGCKGRLICYTSVKWNET 622

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RESULT 15
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QY 1 LLSWGCKGRVLCYTSVQWNST 22

Search completed: May 29, 2003, 11:03:57  
Job time : 20.0317 secs

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GenCure version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:06 (Search time 10.8254 seconds)

(without alignments)  
195,370 Million cell updates/sec

Title: US-09-147-362a-4

Perfect score: 126

Sequence: 1 LLSMCKGRALVCTSYVQNMST 22

Scoring table: BIOSCM62

Gapped 10.0, Gapext 0.5

Searched: 283224 seqs, 9613442 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: PIR-73.\*

1: P121.\*

2: P122.\*

3: P123.\*

4: P124.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	108	85.7	863	2 A53034	gag polyprotein -
2	108	85.7	863	2 A53034	envelope protein p
3	101	89.2	104	2 S52930	GPI1 ENV protein g
4	85	87.5	358	2 S22002	envelope protein g
5	85	87.5	443	2 C41621	envelope protein g
6	85	87.5	853	2 S54384	envelope glycoprote
7	85	87.5	853	2 S54384	envelope glycoprote
8	85	87.5	853	2 S54384	envelope glycoprote
9	85	87.5	853	2 S54384	envelope glycoprote
10	85	87.5	853	2 S54384	envelope glycoprote
11	85	87.5	853	2 S54384	envelope glycoprote
12	85	87.5	853	2 S54384	envelope glycoprote
13	85	87.5	853	2 S54384	envelope glycoprote
14	85	87.5	853	2 S54384	envelope glycoprote
15	85	87.5	853	2 S54384	envelope glycoprote
16	85	87.5	853	2 S54384	envelope glycoprote
17	85	87.5	853	2 S54384	envelope glycoprote
18	85	87.5	853	2 S54384	envelope glycoprote
19	85	87.5	853	2 S54384	envelope glycoprote
20	85	87.5	853	2 S54384	envelope glycoprote
21	85	87.5	853	2 S54384	envelope glycoprote
22	85	87.5	853	2 S54384	envelope glycoprote
23	85	87.5	853	2 S54384	envelope glycoprote
24	85	87.5	853	2 S54384	envelope glycoprote
25	85	87.5	853	2 S54384	envelope glycoprote
26	85	87.5	853	2 S54384	envelope glycoprote
27	85	87.5	853	2 S54384	envelope glycoprote
28	85	87.5	853	2 S54384	envelope glycoprote
29	85	87.5	853	2 S54384	envelope glycoprote

30	82	65.1	856	1 A44963	env polyprotein pr
31	82	65.1	859	1 VCLJMN	env polyprotein pr
32	82	65.1	861	1 VCLJIV	env polyprotein pr
33	82	65.1	861	1 VCLJSC	env polyprotein pr
34	82	65.1	861	1 VCLJSC	env polyprotein pr
35	81	64.3	846	1 VCLJND	env polyprotein pr
36	80	63.5	786	2 S28084	env polyprotein pr
37	76.5	60.7	151	2 S30448	env protein - huma
38	76.5	60.7	151	2 S30453	env protein - huma
39	76.5	60.7	151	2 S30452	env protein - huma
40	76.5	60.7	151	2 S30450	env protein - huma
41	76.5	60.7	151	2 S30450	env protein - huma
42	76.5	60.3	729	1 VCLJXZ	env protein - huma
43	76	60.3	859	2 T01672	envelope glycoprote
44	75	59.5	861	2 VCLJMB	env polyprotein pr
45	75	59.5	861	2 S33985	env polyprotein pr

## ALIGNMENTS

## RESULT 1

A53034 gag polyprotein - human immunodeficiency virus type 1 (strain Ane70)

C/Spectrum: human immunodeficiency virus type 1, HIV-1

C/Date: 03-May-1994 #sequence\_revision 03-May-1994 #ext\_change 07-May-1995

R/Vanden Haevevalde, M.; Decourt, J.L.; De Leyn, R.J.; Vanderborght, B.; Van der Groen,

J. VIROL. 68, 1565-1596, 1994

A/Title: Genomic cloning and complete sequence analysis of a highly divergent African hu

A/Reference number: A53034, MUID:94149849, PMID:8107220

A/Accession: A53034

A/Status: Preliminary

A/Release type: Genomic RNA

A/Release type: Genomic RNA

A/Cross-reference: GB102587

A/Cross-reference: GB102587

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A/Cross-reference: GB102587

C>Date: 20-Feb-99 #sequence revision  
C/Accession: S22002; 570418  
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
Submitted to the EMBL Data Library, July 1991  
A/Purpose: Isolation of HIV-1 in blood and cerebrospinal fluid as determinant of viral tropism  
A/Accession: S22002  
A/Molecule type: DNA  
A/Residues: 1-358 <STE>  
A/Cross-references: EMBL:X61352; NID:g60186; PID:CAA3616.1; PTD:G60187  
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
A/Res. Des.: Rev. Reviews 6/3/95, 1992 Immunodeficiency virus type 1 in blood and cerebrospinal fluid  
A/Reference number: S70417; MUID:92144209; PMID:11736940  
A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1-333.'X'.335-358.<STE>  
A/Cross-references: EMBL:X61352; NID:g60186  
C/Superfamily: type E retrovirus env polyprotein

Query Match 67.5% Score 85; DB 2 Length 358;  
Best Local Similarity 59.1%; Pred. No. 0.00011;  
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 1 LLSMCKGRGLVCTYSVMNST 22  
||| ||| ||| ||| ||| ||| :|||  
Db 94 LLGIWCGSKRLCTTVAVPNMS 115

RESULT 6  
CA1621  
env polyprotein p - human immunodeficiency virus type 1 (fragment)  
N/Antigenic names: coat polyprotein  
N/Contexts: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C/Spectrum: human immunodeficiency virus type 1, HIV-1  
C/Data: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C/Accession: CA1621  
R/Burger, H.; Meiler, B.; Flaherty, K.; Guille, J.; Nguyen, P.N.; Gibba, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
A/Reference number: A41621; MUID:92107924; PMID:1763038  
A/Occasion: C41621  
A/Accession: CA1621  
A/Residues: 1-1443 <HNP>  
A/Cross-references: GB:M77230; NID:g328631; PIND:AAB03792.1; PID:g555015  
A>Note: this virtue was isolated from the mother's sexual partner  
C/Genetics:

A/Gene: env  
C/Superfamily: type E retrovirus env polyprotein  
A/Protein name: polyprotein, immunodeficiency; polyprot  
F/SeqType/Product: coat protein gp120 (fragment) #status predicted <cp1>  
F/Size/Length/Product: coat protein gp41 (fragment) #status predicted <cp2>  
F/seq443/Domains: transmembrane #status predicted <TM>  
F/9,123,36,68,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 67.5% Score 85; DB 2 Length 443;  
Best Local Similarity 59.1%; Pred. No. 0.00013;  
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 1 LLSMCKGRGLVCTYSVMNST 22  
||| ||| ||| ||| ||| ||| :|||  
Db 332 LLGIWCGSKRLCTTVAVPNMS 353

RESULT 7  
SS4384  
env polyprotein - human immunodeficiency virus type 1  
C/Spectrum: human immunodeficiency virus type 1, HIV-1  
C/Data: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999  
C/Accession: SS4384  
C/Theodore, T.; Buckler-White, A.J.

submitted to the EMBL Data Library, July 1989

A:Accession: S54377  
A:Accession: S54377  
A:Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-853 <THE>  
A:Cross-references: EMBL:M22639; NID:G329377; PID:AAA45370.1; PID:G329385  
C:Superfamily: type B retrovirus env polypotein  
C:Keyword: polypotein

Query Match 67.5%; Score 85; DB 2; Length 853;

Best Local Similarity 59.1%; Pred. No. 0.00023;  
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLSWGCGRKLVCTYSVQVNST 22  
DB 591 LLSWGCGRKLVCTYSVQVNST 610

RESULT 8

env polypotein precursor - simian immunodeficiency virus STVcpz  
N:Alternate names: coat polypotein  
N:Context: coat protein gp120; coat protein gp41  
C:Species: simian immunodeficiency virus STVcpz  
C:Accession: S22000  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #ext\_change 16-Jul-1999  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Haecke, W.  
R:Hueter, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Main-Hobson, S.  
N:ature 345, 356-359, 1990  
A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.  
A:Reference number: S095983; MUID:9025077; PMID:2188136  
A:Accession: S22000  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-854 <HUE>  
A:Cross-references: EMBL:X52154; NID:G59866; PID:CAA36407.1; PID:G598674  
C:Superfamily: type B retrovirus env polypotein  
C:Keyword: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypotein  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-500/Product: coat protein gp120 #status predicted <CP1>  
F:501-854/Product: coat protein gp41 #status predicted <CP2>  
F:501-517/Domain: transmembrane #status predicted <TM1>  
F:675-693/Domain: transmembrane #status predicted <TM2>  
F:685-821/Domain: transmembrane #status predicted <TM3>  
F:140-149,151,155,158,166,195,239,260,267,274,299,331,335,351,356,384,392,426,432,446,45

Best Local Similarity 67.5%; Score 85; DB 1; Length 854;  
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLSWGCGRKLVCTYSVQVNST 22  
DB 592 LLSWGCGRKLVCTYSVQVNST 603

RESULT 9

env polypotein precursor - human immunodeficiency virus Zr-6  
N:Alternate names: coat polypotein  
N:Context: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus Zr-6  
C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1997 #ext\_change 16-Jul-1999  
C:Accession: D26192  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
R:Hueter, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Main-Hobson, S.  
N:ature 345, 356-359, 1990  
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleic acid sequence and protein structure  
A:Reference number: A21932; MUID:8724097; PMID:303660  
A:Accession: D26192  
A:Molecule type: DNA  
A:Residues: 1-855 <SRI>  
A:Cross-references: GB:K03458; GB:ML6322; NID:G329398; PID:AAA45380.1; PID:G329403

C:Genetics:

C:Superfamily: type B retrovirus env polypotein  
C:Keyword: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypotein  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-500/Product: coat protein gp120 #status predicted <CP1>  
F:501-855/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:501-517/Domain: transmembrane #status predicted <TM1>  
F:675-693/Domain: transmembrane glycoprotein #status predicted <TM2>  
F:140-149,151,155,158,166,195,239,260,267,274,299,331,335,351,356,384,392,426,432,446,45

Query Match 67.5%; Score 85; DB 1; Length 855;

Best Local Similarity 59.1%; Pred. No. 0.00023;  
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLSWGCGRKLVCTYSVQVNST 22  
DB 591 LLSWGCGRKLVCTYSVQVNST 612

RESULT 10

envelope protein gp120/gp41 - human immunodeficiency virus type 1  
N:Accession: S22000  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #ext\_change 12-Apr-1995  
C:Accession: S22000  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Haecke, W.  
R:Hueter, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Main-Hobson, S.  
N:ature 345, 356-359, 1990  
A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.  
A:Reference number: S095983; MUID:9025077; PMID:2188136  
A:Accession: S22000  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-358 <STE>  
A:Cross-references: EMBL:X61351  
C:Superfamily: type B retrovirus env polypotein  
C:Keyword: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypotein  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-500/Product: coat protein gp120 #status predicted <CP1>  
F:501-855/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:501-517/Domain: transmembrane #status predicted <TM1>  
F:675-693/Domain: transmembrane glycoprotein #status predicted <TM2>  
F:140-149,151,155,158,166,195,239,260,267,274,299,331,335,351,356,384,392,426,432,446,45

Query Match 66.7%; Score 84; DB 2; Length 358;

Best Local Similarity 59.1%; Pred. No. 0.00015;  
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 LLSWGCGRKLVCTYSVQVNST 22  
DB 94 LLSWGCGRKLVCTYSVQVNST 115

RESULT 11

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment  
N:Accession: S22000  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #ext\_change 12-Apr-1995  
C:Accession: S22000  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
R:Hueter, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Main-Hobson, S.  
N:ature 345, 356-359, 1990  
A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.  
A:Reference number: S095983; MUID:9025077; PMID:2188136  
A:Accession: S22000  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-358 <STE>  
A:Cross-references: EMBL:X61351; NID:G60184; PID:CAA3614.1; PID:G60185  
C:Superfamily: type B retrovirus env polypotein  
C:Keyword: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypotein  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-500/Product: coat protein gp120 #status predicted <CP1>  
F:501-855/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:501-517/Domain: transmembrane #status predicted <TM1>  
F:675-693/Domain: transmembrane glycoprotein #status predicted <TM2>  
F:140-149,151,155,158,166,195,239,260,267,274,299,331,335,351,356,384,392,426,432,446,45

Query Match 66.7%; Score 84; DB 2; Length 358;

Best Local Similarity 59.1%; Pred. No. 0.00015;  
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 LLSWGCGRKLVCTYSVQVNST 22  
DB 94 LLSWGCGRKLVCTYSVQVNST 115

RESULT 12

```

522006
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 26-Aug-1999
C:Accession: S70420; S62006
R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1136940
A:Accession: S70420
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STE2>
A:Cross-references: EMBL:X61354; NID:g60190; PIDN:CAA43620.1; PID:g60191
A:Experimental source: patient L, Data Library, July 1991
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type B retrovirus env polyprotein
Query Match 65.1%; Score 82; DB 2; Length 357;
Best Local Similarity 54.5%; Pred. No. 0.00029;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 LLSWGCKGRJVCYVSQVNST 22
DB 93 LIGWCSGKRLICTTVPMNNTS 114

RESULT 13
521994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 01-Dec-2000
C:Accession: S21994; S70421
R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
A:Reference number: S21990
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180
R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1136940
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140; 'X', 142-312; 'X', 314-357 <STE2>
A:Cross-references: EMBL:X61355; NID:g60179
A:Superfamily: type B retrovirus env polyprotein
Query Match 65.1%; Score 82; DB 2; Length 357;
Best Local Similarity 54.5%; Pred. No. 0.00029;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 LLSWGCKGRJVCYVSQVNST 22
DB 93 LIGWCSGKRLICTTVPMNNTS 114

RESULT 14
522004
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 4B
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 01-Dec-2000
C:Accession: S22004; S62006
R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
A:Reference number: S21990

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A:Accession: S22004
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61353; NID:g60188; PIDN:CAA43618.1; PID:g60189
R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1136940
A:Accession: S70419
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-292; 'X', 294-357 <STE2>
A:Cross-references: EMBL:X61353; NID:g60188
A:Superfamily: type B retrovirus env polyprotein
Query Match 65.1%; Score 82; DB 2; Length 357;
Best Local Similarity 54.5%; Pred. No. 0.00029;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 LLSWGCKGRJVCYVSQVNST 22
DB 93 LIGWCSGKRLICTTVPMNNTS 114

RESULT 15
521996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 26-Aug-1999
C:Accession: S70422; S21996
R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1136940
A:Accession: S70422
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STE2>
A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129
A:Experimental source: patient 27L
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type B retrovirus env polyprotein
Query Match 65.1%; Score 82; DB 2; Length 357;
Best Local Similarity 54.5%; Pred. No. 0.00029;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 LLSWGCKGRJVCYVSQVNST 22
DB 93 LIGWCSGKRLICTTVPMNNTS 114

Search completed: May 29, 2003, 10:40:24
CDD time : 11.824 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:31:50 / Search time 5.4127 Seconds

(without alignments)  
168,581 Million cell updates/sec

Title: US-09-147-362a-4

Perfect score: 126

Sequence: 1 LLSWGCKRLVCTSYQNMNST 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 segs, 41476328 residues

1 number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
sequence as similar to the query as the best hit being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	67.5	853	1 ENV_HVJ22	P12497 human immun
2	85	67.5	854	1 ENV_HVJ22	P12497 human immun
3	85	67.5	854	1 ENV_HVJ22	P12497 human immun
4	82	65.1	843	1 ENV_HVJ22	P12497 human immun
5	82	65.1	847	1 ENV_HVJ22	P12497 human immun
6	82	65.1	847	1 ENV_HVJ22	P12497 human immun
7	82	65.1	851	1 ENV_HVJ22	P12497 human immun
8	82	65.1	852	1 ENV_HVJ22	P12497 human immun
9	82	65.1	853	1 ENV_HVJ22	P12497 human immun
10	82	65.1	853	1 ENV_HVJ22	P12497 human immun
11	82	65.1	853	1 ENV_HVJ22	P12497 human immun
12	82	65.1	855	1 ENV_HVJ22	P12497 human immun
13	82	65.1	856	1 ENV_HVJ22	P12497 human immun
14	82	65.1	856	1 ENV_HVJ22	P12497 human immun
15	82	65.1	856	1 ENV_HVJ22	P12497 human immun
16	82	65.1	856	1 ENV_HVJ22	P12497 human immun
17	82	65.1	856	1 ENV_HVJ22	P12497 human immun
18	82	65.1	856	1 ENV_HVJ22	P12497 human immun
19	82	65.1	856	1 ENV_HVJ22	P12497 human immun
20	82	65.1	856	1 ENV_HVJ22	P12497 human immun
21	82	65.1	856	1 ENV_HVJ22	P12497 human immun
22	82	65.1	856	1 ENV_HVJ22	P12497 human immun
23	82	65.1	856	1 ENV_HVJ22	P12497 human immun
24	82	65.1	856	1 ENV_HVJ22	P12497 human immun
25	82	65.1	856	1 ENV_HVJ22	P12497 human immun
26	82	65.1	856	1 ENV_HVJ22	P12497 human immun
27	80	63.5	848	1 ENV_HVJ22	P12497 human immun
28	80	63.5	848	1 ENV_HVJ22	P12497 human immun
29	80	63.5	848	1 ENV_HVJ22	P12497 human immun
30	78	61.9	853	1 ENV_HVJ22	P12497 human immun
31	78	61.9	853	1 ENV_HVJ22	P12497 human immun
32	78	61.9	853	1 ENV_HVJ22	P12497 human immun
33	74	58.7	857	1 ENV_HVJ22	P12497 human immun

34	72.5	57.5	856	1 ENV_HVJ22	P05883 human immun
35	71.5	55.2	856	1 ENV_HVJ22	P05883 human immun
36	69.5	55.2	856	1 ENV_HVJ22	P12497 human immun
37	69.5	55.2	856	1 ENV_HVJ22	P12497 human immun
38	69.5	55.2	856	1 ENV_HVJ22	P12497 human immun
39	69.5	55.2	856	1 ENV_HVJ22	P12497 human immun
40	69.5	55.2	856	1 ENV_HVJ22	P12497 human immun
41	69.5	55.2	856	1 ENV_HVJ22	P12497 human immun
42	69.5	55.2	856	1 ENV_HVJ22	P12497 human immun
43	69.5	55.2	856	1 ENV_HVJ22	P12497 human immun
44	69.5	55.2	856	1 ENV_HVJ22	P12497 human immun
45	69.5	55.2	856	1 ENV_HVJ22	P12497 human immun

## ALIGNMENTS

RESULT 1	ID	ENV_HVJ22	STANDARD	PRT	853 AA
AC	P12497				
DT	01-OCT-1989 (Rel. 12, Created)				
DT	01-OCT-1989 (Rel. 12, Last sequence update)				
DT	16-OCT-1989 (Rel. 40, Last annotation update)				
DT	Envelope polypeptide (p160 precursor) [contaminant: Envelope membrane				
CM	ENV_HVJ22 (GPI20), Transmembrane glycoprotein (GPI41).				
OS	Human immunodeficiency virus type 1 (22/CDC-234 isolate) (HIV-1).				
OC	Vitruvius; Retroviral virus; Retroviral; Lentivirus.				
NCBI	Taxid:11683				
RE	SEQUENCE FROM N.A. (see below)				
RE	Submitted (Nov-1988) to the HIV data bank.				
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CC	entities requires a license agreement (see <a href="http://www.ftp.ebi.ac.uk/announce/">http://www.ftp.ebi.ac.uk/announce/</a>				
CC	EMBL, M2639; AAA5370.1; -				
DR	HIV; M2639; ENV5226.				
DR	InterPro; IPR000328; GP120.				
DR	Pfam; PF00516; GP120; 1.				
CC	Alam; P00517; GP120; 1.				
KW	Signal.				
FT	CHAIN	1..31			
FT	DISULFID	53..73			
FT	DISULFID	118..126			
FT	DISULFID	133..144			
FT	DISULFID	154..164			
FT	DISULFID	219..248			
FT	DISULFID	229..240			
FT	DISULFID	297..330			
FT	DISULFID	376..442			
FT	DISULFID	383..415			
FT	DISULFID	857..877			
FT	CARBOHYD	137..153			
FT	CARBOHYD	144..153			
FT	CARBOHYD	153..153			
FT	CARBOHYD	157..157			
FT	CARBOHYD	185..185			
FT	CARBOHYD	188..188			
FT	CARBOHYD	198..198			
FT	CARBOHYD	208..208			
FT	CARBOHYD	242..242			

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FT CARBOHYD 263 263 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 277 277 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 290 290 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 296 296 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 331 331 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 338 338 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 353 353 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 359 359 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 390 390 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 402 402 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 441 441 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 445 445 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 458 458 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 459 459 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 468 468 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 613 613 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 622 622 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 634 634 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 671 671 N-LINKED (GLCNAC...) (POTENTIAL)
SEQUENCE 853 AA; 97043 MW; 8490808CAF7008 CRC64;

Query Match 67.5%; Score 85; DB 1; Length 853;
Best Local Similarity 59.1%; Pct Ident 2; Pct Ident 0;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 LLSWGGCKRGRLVCYGVONST 22
DB 589 LGLMGCSKRLCTTVPMNS 610

RESULT 2
ENV_SIVCZ STANDARD; PRT; 854 AA.
ID ENV_SIVCZ STANDARD; PRT; 854 AA.
AC P17281;
AC 01-AUG-1990 (rel. 15, Created)
DT 01-AUG-1990 (rel. 15, Last sequence update)
DE 15-JUL-1999 (rel. 18, Last sequence update)
DE Envelope polypeptide GP160 precursor (containing: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
GN ENV.
OS Chimpanzee immunodeficiency virus (SIV/cpz1) (CIV).
SV Virus; Retroid viruses; Retroviridae; Lentivirus.
RN [1] TaxID:1173;
RP SEQUENCE FROM N.A.
RU HuET.T., Chevalier R., Meyerhan A., Roelants G., Main-Hobson S.;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
Nucleic Acids Res. 1990; 18(1):359-369.
CC -1. SIMILARITY: STRONG, WITH HIV-1 ENV POLYPROTEIN.
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CC
CC EMBL: X53154; CAA6407.1;
CC PIR: S09990; VCLJ2R.
CC DR HIV; X53154; ENVSICPZ.
CC DR InterPro: IPR000328; ENV_GP41.
CC DR Pfam: PF00516; GP120; 1.
CC DR AIDS; Coe Protein; polypeptide; glycoprotein; Transmembrane;
CC Signal.
CC FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
CC FT CHAIN 31 500 TRANSMEMBRANE GLYCOPROTEIN.
CC FT TRANSMEM 501 517 POTENTIAL.

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FT TRANSMEM 675 693 POTENTIAL.
FT TRANSMEM 693 693 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 135 134 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 140 140 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 143 143 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 154 154 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 158 158 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 187 187 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 215 215 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 260 260 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 267 267 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 274 274 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 299 299 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 331 331 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 356 356 N-LINKED (GLCNAC...) (POTENTIAL)
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FT CARBOHYD 384 384 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 426 426 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 432 432 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 446 446 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 460 460 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 608 608 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 628 628 N-LINKED (GLCNAC...) (POTENTIAL)
SEQUENCE 854 AA; 95803 MW; 2E249FAD4F2D9B3 CRC64;

Query Match 67.5%; Score 85; DB 1; Length 854;
Best Local Similarity 59.1%; Pct Ident 2; Pct Ident 0;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 LLSWGGCKRGRLVCYGVONST 22
DB 582 LGLMGCSKRLCTTVPMNS 603

RESULT 3
ENV_HV126 STANDARD; PRT; 855 AA.
ID ENV_HV126 STANDARD; PRT; 855 AA.
AC P04560;
AC 13-AUG-1987 (rel. 05, Created)
DT 13-AUG-1987 (rel. 05, Last sequence update)
DE 13-AUG-1987 (rel. 05, Last sequence update)
DE Envelope polypeptide GP160 precursor (containing: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
SV Virus; Retroid viruses; Retroviridae; Lentivirus.
RN [1] TaxID:11708;
RP SEQUENCE FROM N.A.
RU MEDLINE:87248097; Pubmed:1036660.
RA Srinivasan A., Anand R., York D., Ranganathan P., Peorino P.,
RA Schochetman G., Curran J., Kalayanaraman V.S., Luciw P.A.,
RA Sanchez-Pescador R.;
RA "Molecular characterization of human immunodeficiency virus from
RA Zaire: nucleotide sequence analysis identifies conserved and variable
RA regions in the envelope gene.";
CC Gene 53:71-82(1987).
CC
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CC
CC EMBL: K03458; AAA45380.1;
CC PIR: D26192; VCLJ2R.

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DR HIV; X03458; ENV526; Env GP41.  
 DR InterPro: IPR000328; GP120.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP41, 1.  
 DR AIDS; Coat protein; Glycoprotein; Transmembrane;  
 signal.  
 KM Signal. 1 30  
 FT CHAIN 511 825  
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 FT DISULFID 118 207  
 FT DISULFID 125 198  
 FT DISULFID 130 155  
 FT DISULFID 220 249  
 FT DISULFID 220 241  
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 FT DISULFID 385 417  
 FT CARBOHYD 87 87  
 FT CARBOHYD 129 129  
 FT CARBOHYD 140 140  
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 FT CARBOHYD 154 154  
 FT CARBOHYD 154 154  
 FT CARBOHYD 186 186  
 FT CARBOHYD 189 189  
 FT CARBOHYD 199 199  
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 SQ SEQUENCE 855 AA; 96971 MW; 3840356239C3457 CRC64;  
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 Best Local Similarity: 59.1%; Pctid. No. 2; 1e-05;  
 Matches 1; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 Oy 1 LLSMSCKRGRVACYTSYVQNS 22  
 Db 591 LIGTIGSCXKLICTTVPMNNS 612  
 RESULT 4  
 ENV\_HVIY2 STANDARD; PRT; 843 AA.  
 AC P31561;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 15-JUN-1994 (Rel. 38, Last sequence update)  
 DI 15-JUN-1999 (Rel. 39, Last annotation update)  
 DE Glycoprotein GP160 precursor (containing: Exterior membrane  
 glycoprotein (GP160), Transmembrane glycoprotein (GP41)).  
 OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).

CC Vlnases; Retroid vlnases; Retroviridae; Lentivirus.  
 OK NCBI\_TaxID=36377;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93021387; PubMed=1404605;  
 RA Li Y., Hui H., Burgess C.J., Price R.W., Hahn B.H.,  
 Shaw G.M.;  
 RT "Complete nucleotide sequence, genome organization, and biological  
 properties of human immunodeficiency virus type 1 in vivo: evidence  
 for limited defectiveness and complementation."  
 CC U. Virol. 66:6587-6607(1992).  
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 email to: [license@sib-sb.ch](mailto:license@sib-sb.ch)).  
 CC EMBL\_M93258; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; H44001; H44001.  
 DR InterPro: IPR000328; Env GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120, 1.  
 DR AIDS; Coat protein; Glycoprotein; Transmembrane;  
 signal.  
 KM Signal. 1 29  
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 FT CHAIN 490 843  
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 FT CARBOHYD 803 803  
 SQ SEQUENCE 843 AA; 95648 MW; C69D97910318B71 CRC64;  
 Query Match Similarity: 54.5%; Score 82; DB-1; Length 843;  
 Best Local Similarity: 54.5%; Pctid. No. 5; 9e-05;

FT	CAROHYD	398	398	N-LINKED (GLCNAC..)	(POTENTIAL).
FT	CAROHYD	401	401	N-LINKED (GLCNAC..)	(POTENTIAL).
FT	CAROHYD	438	438	N-LINKED (GLCNAC..)	(POTENTIAL).
FT	CAROHYD	456	456	N-LINKED (GLCNAC..)	(POTENTIAL).
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SQ	SEQUENCE	847 AA:	96135 MW;	0.690117	DPF22B_CK64;

Query Match: 65.1%, Score 82; DB 1; Length 847;  
Best Local Similarity: 59.3%; Fred. Size=02;  
Matched 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0.

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		:           :	
		583 LLLGGTSCSLGKLCTTAVDPMNAS 604	

RESULT 6  
ENV\_HIVWJ2 STANDARD; PRI: 847 AA.  
ID ENV\_HIVWJ2  
POS580;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DE 15-VUL-1999 (Rel. 38, Last annotation update)  
DE ENVELOPE POLYPEPTIDE GP160 precursor [Contains: Exterior membrane glycoprotein (GP120), transmembrane glycoprotein (GP41)].  
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirae.  
NCBI\_TaxId=11705;  
RN [1]  
RS SEQUENCE FROM N.A.  
RX MEDLINE=86233430; PubMed=3011778;  
RA Smith R.D., Montefiori D.E., Redfield R.B., Marham P.D., Berman J.S., Johnson V.A., Wong-Staal F., Gallo R.C., Parks W.P.;  
RT "Genomic variation in HIV-II/LAV over time in patients with AIDS or at risk for AIDS.";  
RL Science 232:1548-1553(1986).  
CC 1.- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SUBMITTALLY TAKEN FROM A TWO-YEAR OLD PAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.  
CC -----  
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DR EMBL: M12507; AB12990.1; -.  
DR HIV: M12507; EVNSMWJ2.  
DR InterPro: IPR000328; ENV\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR KEGG: Coat protein; Polypeptin; Glycoprotein; Transmembrane; S100; S100L; K01101.  
FT FT CHAIN 30 501 29  
FT CHAIN 1 502 847 EXTERIOR MEMBRANE GLYCOPROTEIN,  
FT DISULFD 53 73 TRANSMEMBRANE GLYCOPROTEIN.  
FT DISULFD 118 202 BY SIMILARITY.  
FT DISULFD 125 202 BY SIMILARITY.  
FT DISULFD 133 202 BY SIMILARITY.  
FT DISULFD 215 244 BY SIMILARITY.  
FT DISULFD 225 236 BY SIMILARITY.  
FT DISULFD 293 326 BY SIMILARITY.  
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CAROHYD 87 87 N-LINKED (GLCNAC.. ) (POTENTIAL).

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SQ SEQUENCE 847 AA, 9646 MW, CD1E33D73BA5BC6 CRC64)

Query Match 65.1%; Score 82; DB 1; Length 847;
Beet Local Similarity 54.5%; Pctd. No. 5.9e-05;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

1 LLSMCKRGRLNCTYSVQNNST 22
583 LLSMCKRGRLNCTYSVQNNST 604

Db 583 LLSMCKRGRLNCTYSVQNNST 604

RESULT 7
ID ENV_HV1B8 STANDARD; PRT; 851 AA.
AC P04582;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contamin: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
DE Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
DE Virus; Retroid viruses; Retroviridae; Lentivirinae.
OX NCBI_TaxID=11684;
RN [1] _SEQUENCE FROM N.A.
RP MEDLINE=6511123; PUBMED=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Baumanter K., Damschke J.A., Whitehorn E.A.,
RA Laubenberg J.A., Papas T.S., Chirgwin J., Chong N.T., Gallo R.C.,
RA Wong-Staal F.;
RL *Complete nucleotide sequence of the AIDS virus, HTLV-III";
RL Nature 313:277-284(1985).
CC The sequence of this entry is copyright. It is produced through a collaboration between the U.S. Department of Health and Human Services and the European Commission. The European Bioinformatics Institute (EMBL) has no way of use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcements/ or send an email to license@ebi.ac.uk).
CC EMBL: X02011.1; MM4661.1;
CC HIV: X02011.1; NS5888;
CC GlycositeDB: P04582; -

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DR InterPro: IPR000328, Env GP41.
DR InterPro: IPR000777, GP120.
DR Pfam: PF00515, GP120; 1.
DR ProDom: PD00111, 1.
DR KEGG: K02011, 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
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FT CHAIN 31 506
FT CHAIN 507 851
FT DISULFID 54 74
FT DISULFID 139 206
FT DISULFID 128 157
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FT DISULFID 218 247
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Query Match 65.1%; Score 82; DB 1; Length 851;
Beet Local Similarity 54.5%; Pctd. No. 5.9e-05;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

1 LLSMCKRGRLNCTYSVQNNST 22
587 LLSMCKRGRLNCTYSVQNNST 608

Db 587 LLSMCKRGRLNCTYSVQNNST 608

RESULT 8
ID ENV_HV1B8 STANDARD; PRT; 852 AA.
AC P1248;
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contamin: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
DE HIV.
DE Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
DE Virus; Retroid viruses; Retroviridae; Lentivirinae.
OX NCBI_TaxID=11693;
RN [1] _SEQUENCE FROM N.A.

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RX MEDLINE=89085611; PubMed=2789516;  
 RA Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Lucif P.,  
 RA Dandekar S.;  
 RA "Biological and molecular characterization of human immunodeficiency  
 RT virus (HIV-188) from the brain of a patient with progressive  
 RT dementia." (69:79-86(1998)).  
 CC -1. MISCELLANEOUS; THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS  
 CC HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.  
 CC  
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 CC  
 CC EMBL; M21098; AAA44221.1;  
 CC  
 CC PIR; A11667; VCLUUR.  
 CC HIV; M10109; ENVSERPA.  
 CC Interpro: IPR000777; GP120.  
 DR Pfam; PF00516; GP120.1.  
 DR Pfam; PF00517; GP41.1.  
 KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 50  
 FT CHAIN 508 852  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
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 FT CARBOHYD 812 812  
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 Query Match 65.1%; Score 82; DB 1; Length 852;  
 Best Local Similarity 54.5%;  
 Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Cy 1 L155WCKGRKVCYGYVONST 22  
 Db 588 LKIGWCKSGKILCTTAAVFNMS 609  
 REQUEST 9  
 ID ENV HV153 STANDARD; PRT; 852 AA.  
 AC P19549;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 16-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Envelope polypeptide glycoprotein (Glycoprotein; Exterior membrane  
 GN polypeptide (GP120); Transmembrane glycoprotein (GP41)).  
 GN HIV-1.  
 OS Human immunodeficiency virus type 1 (SP1 isolate) (HIV-1).  
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.  
 NC NCBI\_TaxID=11690;  
 RN (1)  
 RX SEQUENCE FROM N.A.  
 RA Rhee S.Y., Thayer R., Srinivasan A., Nayyar S., Gardner M., Lucif P.,  
 RA Dandekar S.;  
 RA "Biological and molecular characterization of human immunodeficiency  
 RT virus (HIV-188) from the brain of a patient with progressive  
 RT dementia." (69:79-86(1998)).  
 CC -1. MISCELLANEOUS; THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS  
 CC HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.  
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 CC  
 CC EMBL; M10109; ENVSERPA.  
 CC Interpro: IPR000777; GP120.  
 DR Pfam; PF00516; GP120.1.  
 DR Pfam; PF00517; GP41.1.  
 KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM Signal.  
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 FT CHAIN 507 852  
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 SQ SEQUENCE 852 AA; 97203 MW; 288665345DEC915F CRC64;  
 Query Match 65.1%; Score 82; DB 1; Length 852;  
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CC	FT	CARBOHYD	156	156	N-LINKED (GLCNAC..)
CC	FT	CARBOHYD	166	166	N-LINKED (GLCNAC..)
CC	FT	CARBOHYD	186	186	N-LINKED (GLCNAC..)
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CC	FT	CARBOHYD	250	260	N-LINKED (GLCNAC..)
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CC	FT	CARBOHYD	287	287	N-LINKED (GLCNAC..)
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CC	Matches	12;	Conservative	5;	Mismatches 5;
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CC					Gaps 0;
CC	Db	1 L15SMCKCEKGVITCTVONKST 22			
CC		590 L15SMCKCEKGVITCTVONKST 611			
CC	ENV_HVIIA2	STANDARD;	PRF;	855 AA.	
CC	AD	P03379;			
CC	IC	ENV_HVIIA2			
CC	21-JUL-1986	(Ref.)	01	Created	
CC	15-JUL-1999	(Ref.)	38	Last annotation update	
CC	Envelope polypeptide gp160 precursor				
CC	glycoprotein (Gp120)				
CC	ENV.				
CC	Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).				
CC	Viruses; Retroviruses; Retroviridae; Lentivirus.				
CC	11	_taxid=11685;			
CC	SEQUENCE FROM N.A.				
CC	MEDLINE=6509453;				
CC	Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,				
CC	Stempien M.M., Brown-Slimer S.L., Gee M.W., Renard A., Randolph A.,				
CC	Lery J.A., Dina D., Lucif P.A.,				
CC	Nucleotide sequence and expression of an AIDS-associated retrovirus				
CC	Science 227:484-492(1985).				
CC	This SMS-S-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	use by non-profit institutions as long as its content is in no way				
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CC	or send an email to: licenses@ebi.ac.uk (see http://www.ebi.ac.uk/comm/				
CC	EMBL; K02007; AA59882.1 -				

CC	OC	Viruses/retroviruses; Retroviridae; Lentivirus.
CC	NCHI_TaxID=11699;	
CC	[1]	
RX	SEQUENCE FROM N.A.	
RN	SEBINE-90148344; Pubmed:2355749;	
RX	"A highly defective G <sub>HVY</sub> retained access	
RT	individual presenting an atypical western blot."	
RL	AIDS 3:707-715(1989)	
CC	-1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A	
CC	HEALTHY GABONENSE INDIVIDUAL.	
CC		
CC	This SWIS-PROT entry is copyright. It is produced through a collaboration	
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CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (see http://www.ebi.ac.uk/commencee/	
CC	or send an email to licenses@ebi.ac.uk).	
CC		
DR	EMBL; M6672; AAA83397.1; -	
DR	InterPro; IPR000328; Env GP41.	
DR	Pfam; PF00516; GP130; 1.	
DR	Pfam; PF00517; GP41; 1.	
KM	Aids; Coat protein; Glycoprotein; Transmembrane;	
KM	signal.	
FT	SIGNAL	1..29
FT	CHAIN	30..539
FT	CHAIN	539..855
FT	DISULFID	53..73
FT	DISULFID	118..210
FT	DISULFID	125..201
FT	DISULFID	130..162
FT	DISULFID	223..232
FT	DISULFID	320..324
FT	DISULFID	381..442
FT	DISULFID	388..415
FT	CARBOHYD	87..87
FT	CARBOHYD	134..134
FT	CARBOHYD	142..142
FT	CARBOHYD	145..145
FT	CARBOHYD	155..155
FT	CARBOHYD	165..161
FT	CARBOHYD	192..192
FT	CARBOHYD	202..202
FT	CARBOHYD	239..239
FT	CARBOHYD	246..246
FT	CARBOHYD	267..267
FT	CARBOHYD	281..281
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FT	CARBOHYD	359..359
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FT	CARBOHYD	458..458
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FT	CARBOHYD	615..615
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FT	CARBOHYD	815..815
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Base Local Similarity 54.5%; Pct Ident 5.9e-05;		
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;		







Query Match 65.1%; Score 82; DB 1; Length 856;  
 Best Local Similarity 54.5%; Pred. No. 6a-05;  
 Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 Oy 1 LLSMCKGRJVCYTSVQNNST 22  
 Db 592 LGIWGCGSKLCTTAVPMWAS 613

Search completed: May 29, 2003, 10:36:58  
 Job time : 5.4127 secs

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US-03-147-60-88

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AC      Q91B95.1
DT      01-OCT-2000 (TrEMBLrel.15, Created)
DT      01-OCT-2000 (TrEMBLrel.15, Last sequence update)
DT      01-DEC-2001 (TrEMBLrel.15, Last annotation update)
DE      Gp41 (fragment).
GN      ENV.
OS      Human immunodeficiency virus type 1.
OC      Viruses; Retrocid viruses; Retroviridae; Lentivirus.
NC      [1]_Taxid:11676.
LN      R.
RP      SEQUENCE FROM N.A.
RC      STRAIN:YF51.
RA      Rodgers P., Robertson D., Sandrine S., Christel D., Francois S.,
RT      Philippe M.;
RT      Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates";
RA      Smith, R. (1994) 1289-52, the EMBL/Genbank/DBD databases.
DR      EMBL:U01642; GenBank:U01642; EMBL:U01642; EMBL:U01642; EMBL:U01642;
DR      InterPro: IP00003285; Env Gp41.
DR      Pfam: PF00517; Gp41; 1_ _Gp41.
DR      Transmembrane.
KV      K.
FT      NON_TER
FT      1
FT      NON_TER
FT      1
SEQUENCE      218 AA; 25243 MW; E7F0E120E579F5A8 CRC64;
Query Match      91.3% Score 115; DE 15; Length 218;
Best Local Similarity 81.8%; Pred No. 3 4e-10;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0
1 LLSMCKCGRLVCTYSVQVNST 22
|||||
54 LLSMCKCGRLVCTYSVQVNST 75

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[illegible]

RESULT 6	
Q9IED5	
ID Q9IED5	PRELIMINARY;
	PRT; 536 AA

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AC 091E05;
DT 01-OCT-2000 (TRENBLREL.15, Created)
DT 01-OCT-2000 (TRENBLREL.15, Last sequence update)
DT 01-DEC-2001 (TRENBLREL.19, Last annotation update)
DE Env Polyprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11676;
NC 111
RP SEQUENCE FROM N.A.
RC STRAIN=YAF31;
RA Rognes P., Robertson D., Damond F., Souquiere S., Mauclet P.,
  Replenne C., Brun-Vezinet F., Dornant D.;
  "HIV-1 group O phylogenetic analysis of C2-GP1 region.",
  Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL: AJ236414; CB96633.1;
  NCBI: U000003.1;
  DR EMBL: AJ236414; CB96633.1;
  DR InterPro: IPR000377; GP120.
PF Pfam: PF00517; GP120; 1.
PE AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER
FT NON_TER 538
SEQUENCE 538 AA; 60777 MW; B3C9B66233FFPD CRC64;

Query Match
Best Local Similarity 91.3%; Score 115; DB 15; Length 538;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRIVCTSYVKNST 22
Db 374 LLSWGCKGRIVCTSYVKNST 395

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RESULT 7
O91DK3 PRELIMINARY; PRT; 214 AA.
AC 091DK3
DT 01-MAR-2001 (TRENBLREL.16, Created)
DT 01-MAR-2001 (TRENBLREL.16, Last sequence update)
DT 01-DEC-2001 (TRENBLREL.19, Last annotation update)
DE Gp1 protein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11676;
NC 111
RP SEQUENCE FROM N.A.
RC STRAIN=BCP120;
RA Rognes P., Robertson D., Damond F., Souquiere S., Mauclet P.,
  Replenne C., Brun-Vezinet F., Dornant D., Simon F.;
  "Phylogenetic analysis of 49 newly derived HIV-1 group O strains: High
  viral diversity but no group M-like subtypes.",
  Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
RL EMBL: AJ293125; CAC1806.1;
  NCBI: U000003.1;
  DR EMBL: AJ293125; CAC1806.1;
  DR InterPro: IPR00517; GP41; 1.
PE Transmembrane.
FT NON_TER
FT NON_TER 1
FT NON_TER 214
SEQUENCE 214 AA; 24436 MW; FFA99D08F61AB8 CRC64;

Query Match
Best Local Similarity 89.7%; Score 113; DB 15; Length 214;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRIVCTSYVKNST 22
Db 45 LLSWGCKGRIVCTSYVKNST 66

```

```

O91E07 PRELIMINARY; PRT; 216 AA.
AC 091E07
DT 01-OCT-2000 (TRENBLREL.15, Created)
DT 01-OCT-2000 (TRENBLREL.15, Last sequence update)
DT 01-DEC-2001 (TRENBLREL.19, Last annotation update)
DE Gp1 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11676;
NC 111
RP SEQUENCE FROM N.A.
RC STRAIN=BCF03;
RA Rognes P., Robertson D., Sandrine S., Christel D., Francois S.,
  Philippe M.;
  "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.",
  Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL: AJ316321; CB96624.1;
  NCBI: U000003.1;
  DR EMBL: AJ316321; CB96624.1;
  DR InterPro: IPR000378; Env GP41.
PF Pfam: PF00517; GP41; 1.
PE Transmembrane.
FT NON_TER
FT NON_TER 1
FT NON_TER 216
SEQUENCE 216 AA; 25015 MW; 780C5F93C6A997C2 CRC64;

Query Match
Best Local Similarity 89.7%; Score 113; DB 15; Length 216;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRIVCTSYVKNST 22
Db 55 LLSWGCKGRIVCTSYVKNST 76

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```

RESULT 9
O91E06 PRELIMINARY; PRT; 234 AA.
AC 091E06
DT 01-OCT-2000 (TRENBLREL.15, Created)
DT 01-OCT-2000 (TRENBLREL.15, Last sequence update)
DT 01-DEC-2001 (TRENBLREL.19, Last annotation update)
DE Gp1 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11676;
NC 111
RP SEQUENCE FROM N.A.
RC STRAIN=YAF32;
RA Rognes P., Robertson D., Sandrine S., Christel D., Francois S.,
  Philippe M.;
  "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.",
  Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL: AJ316321; CB96624.1;
  NCBI: U000003.1;
  DR EMBL: AJ316321; CB96624.1;
  DR InterPro: IPR000378; Env GP41.
PF Pfam: PF00517; GP41; 1.
PE Transmembrane.
FT NON_TER
FT NON_TER 1
FT NON_TER 234
SEQUENCE 234 AA; 26737 MW; 34CFDB999DEFB82 CRC64;

Query Match
Best Local Similarity 89.7%; Score 113; DB 15; Length 234;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLSWGCKGRIVCTSYVKNST 22
Db 62 LLSWGCKGRIVCTSYVKNST 83

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DB 39 L1MSGCKGRILCYTSVQNNKT 60

RESULT 14

ID 091H09 PRELIMINARY; PRT; 130 AA.

AC 091H09; 01-OCT-2000 (FEMBELrel. 15. Created)

DT 01-OCT-2000 (FEMBELrel. 15. Last sequence update)

DE Envelope glycoprotein (Fragment).

GN Gp1.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI TaxID=11676;

RC STRAIN=97CW798;

RE MEDLINE=2036754; PubMed=10931623;

YANG C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,

Pieniazek D., Schable C., Lai R.B.,

"Phylogenetic analysis of protease and transmembrane regions of HIV

type 1 group O."

EMBL=AF2235; RefSeq=U05122

DR InterPro: IPR001326; Pfam: PF00517; Gp1.1\_Gp41.

KM Transmembrane. 1

FT NON\_TER 130

SO SEQUENCE 130 AA; 15593 MW; 5385789A36344EA CRC64;

Query Match

Best Local Similarity 88.9%; Score 112; DB 15; Length 130;

Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 40 L1MSGCKGRILCYTSVQNNKT 61

QY 1 L1MSGCKGRILCYTSVQNNKT 22

DB 40 L1MSGCKGRILCYTSVQNNKT 61

RESULT 15

QJIECI PRELIMINARY; PRT; 183 AA.

AC 091ECL; 01-OCT-2000 (FEMBELrel. 15. Created)

DT 01-OCT-2000 (FEMBELrel. 15. Last sequence update)

DE Gp1 (Fragment).

ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI TaxID=11676;

RC STRAIN=BCP101;

RE MEDLINE=2036754; PubMed=10931623;

YANG C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,

Pieniazek D., Schable C., Lai R.B.,

"Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."

EMBL=AF2235; RefSeq=U05122

DR InterPro: IPR001326; Pfam: PF00517; Gp1.1\_Gp41.

KM Transmembrane. 1

FT NON\_TER 183

SO SEQUENCE 183 AA; 21722 MW; C2A28A73540C8AA CRC64;

Query Match

Best Local Similarity 88.9%; Score 112; DB 15; Length 183;

Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 L1MSGCKGRILCYTSVQNNKT 22

DB 42 L1MSGCKGRILCYTSVQNNKT 63

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Job time : 23.6984 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:30:20 / Search time 29.333 Seconds

(without alignment)

Title: US-09-147-362a-5

Sequence: 1 LLOSGCKRGLVCTSYVMNST 22

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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22: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT.*
23: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a  
greater than or equal to the score of the result being printed,  
and is derived by analysis of the score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	22	19	AA080463	Peptide derived fr
2	122	96.1	22	AA080462	Peptide derived fr
3	118	92.9	22	AA080461	Peptide derived fr
4	115	90.6	22	AA080465	Peptide derived fr
5	114	89.6	40	AA073446	Partial sequence o
6	112	88.2	40	AA073522	Partial sequence o
7	111	87.4	22	AA080463	Peptide derived fr
8	111	87.4	41	AA055561	Partial sequence o
9	111	87.4	113	AA05562	Partial sequence o
10	111	87.4	715	AA05625	HIV-1 group O isol

11	110	86.6	33	21	AA012212	Partial sequence o
12	110	86.6	113	20	AA055559	HIV-1 group O isol
13	109	85.8	32	29	AA080460	Peptide derived fr
14	109	85.8	32	29	AA080460	Peptide derived fr
15	109	85.8	40	17	AA073441	Partial sequence o
16	109	85.8	40	17	AA073441	Partial sequence o
17	109	85.8	41	17	AA073444	Partial sequence o
18	109	85.8	41	17	AA073444	Partial sequence o
19	108	85.0	117	20	AA055548	HIV-1 group O isol
20	107	84.3	22	19	AA080464	Peptide derived fr
21	107	84.3	22	19	AA080464	Peptide derived fr
22	107	84.3	33	20	AA055522	HIV-1 group O env
23	107	84.3	113	20	AA055550	HIV-1 group O env
24	107	84.3	113	20	AA055550	HIV-1 group O env
25	107	84.3	200	21	AA073773	HIV-1 group O env
26	107	84.3	215	20	AA094999	Recombinant pCO-8P
27	107	84.3	215	20	AA094999	Recombinant pCO-8P
28	107	84.3	215	20	AA094999	Recombinant pCO-8P
29	107	84.3	215	20	AA094999	Recombinant pCO-8P
30	107	84.3	215	20	AA094999	Recombinant pCO-8P
31	107	84.3	215	20	AA094999	Recombinant pCO-8P
32	107	84.3	215	20	AA094999	Recombinant pCO-8P
33	107	84.3	373	20	AA094995	HIV-1 group O env
34	107	84.3	373	20	AA094995	HIV-1 group O env
35	107	84.3	460	20	AA095900	Recombinant pCO-11
36	107	84.3	460	20	AA095900	Recombinant pCO-11
37	107	84.3	460	20	AA095900	Recombinant pCO-11
38	107	84.3	460	20	AA095900	Recombinant pCO-11
39	107	84.3	460	20	AA095900	Recombinant pCO-11
40	107	84.3	460	20	AA095900	Recombinant pCO-11
41	107	84.3	490	20	AA094994	HIV-1 group O env
42	107	84.3	490	20	AA094994	HIV-1 group O env
43	107	84.3	490	20	AA094994	HIV-1 group O env
44	107	84.3	490	20	AA094994	HIV-1 group O env
45	107	84.3	618	20	AA095905	Recombinant pCO-9C

#### ALIGNMENTS

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RESULT 1
AA080463
AA080463 standard; peptide: 22 aa.
AC AA080463;
XX
XX 28-JAN-1999 (first entry)
XX
XX Peptide derived from a conserved sequence of group O human HIV.
XX
XX Group O human immune deficiency virus; HIV; detection; infection.
OS
XX Synthetic.
XX Immune deficiency virus.
XX
XX W09845323-A1.
XX
XX 15-OCT-1998.
XX
XX 05-APR-1998. 98WO-FR00691.
XX
XX 24-FEB-1998. 98FR-0002212.
XX
XX 09-APR-1997. 97FR-0004356.
XX
XX (SNP) PASTER SMOFI DYNASTICS SA.
XX
XX Cheneaux DBM, Delagrange JFH, Gabelle SJX, Reunier FY;
XX
XX WPI: 1998-583190/49.
XX
XX New synthetic peptide(s) - useful for, e.g. detecting infection by
XX
XX human immune deficiency virus of group O
```

BS Claim 6: Page 42; 55pp; French.  
 CC AA80459-74 represent synthetic peptides (either linear or cyclized by  
 CC Cys-Cys diethylphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 XX

SO Sequence 22 AA:

Query Match 100.0%; Score 127; DB 19; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 5e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 1 LLSWGCKRGLVCTSYVNNSF 22  
 DB 1 LLSWGCKRGLVCTSYVNNSF 22

AA80462

AA80462 standard; peptide; 22 AA.

AA80462;

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

MO9845323-A1.

15-OCT-1998.

06-APR-1998; 98WO-FR00691.

24-FEB-1998; 98PR-0002212.

09-APR-1997; 97PR-0004356.

(SNP) PASTEUR SANOPI DIAGNOSTICS SA.

Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

WPI; 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by

human immune deficiency virus of group O

Claim 6; Page 42; 55pp; French.

AA80459-74 represent synthetic peptides (either linear or cyclized by

Cys-Cys diethylphide bonds). The peptides represent variable sequences

connected around short highly conserved sequences present in isolates

of group O human immune deficiency virus (HIV). The peptides are

useful as immunological reagents for detecting infection by group O

human immune deficiency virus (HIV).

SO Sequence 22 AA:

Query Match 96.1%; Score 122; DB 19; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 2.2e-09;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

OY 1 LLSWGCKRGLVCTSYVNNSF 22  
 DB 1 LLSWGCKRGLVCTSYVNNSF 22

RESULT 3

ID AA80461 standard; peptide; 22 AA.

AA80461;

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

MO9845323-A1.

15-OCT-1998.

06-APR-1998; 98WO-FR00691.

24-FEB-1998; 98PR-0002212.

09-APR-1997; 97PR-0004356.

(SNP) PASTEUR SANOPI DIAGNOSTICS SA.

Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

WPI; 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by

human immune deficiency virus of group O

Claim 6; Page 42; 55pp; French.

AA80459-74 represent synthetic peptides (either linear or cyclized by

Cys-Cys diethylphide bonds). The peptides represent variable sequences

connected around short highly conserved sequences present in isolates

of group O human immune deficiency virus (HIV). The peptides are

useful as immunological reagents for detecting infection by group O

human immune deficiency virus (HIV).

SO Sequence 22 AA:

Query Match 92.9%; Score 118; DB 19; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 7.5e-09;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

OY 1 LLSWGCKRGLVCTSYVNNSF 22  
 DB 1 LLSWGCKRGLVCTSYVNNSF 22

RESULT 4

ID AA80466 standard; peptide; 22 AA.

AA80466;

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

MO9845323-A1.

15-OCT-1998.

06-APR-1998; 98WO-FR00691.

XX 24-FEB-1998; 98FR-000232.  
 XX 09-APR-1997; 97FR-0001356.  
 XX (SNFI) PASTERIS SANOFI DIAGNOSTICS SA.  
 XX Chenbaux DMB, Delaigneau JFH, Gabelle SUX, Rieunier FY;  
 XX WPI: 1998-583190/49.  
 XX New synthetic peptide(s) - useful for e.g. detecting infection by  
 XX human immune deficiency virus of group O  
 XX Claim 6; Page 43; 55pp; French.  
 XX AM80459-74 represent synthetic peptides (either linear or cyclised by  
 XX C-terminal amide bonds). The peptides represent variable sequences  
 XX of group O human immune deficiency virus (HIV). The peptides are  
 XX useful as immunological reagents for detecting infection by group O  
 XX human immune deficiency virus (HIV).

S0 Sequence 22 AA;  
 Query Match 90.6%; Score 115; DB 10; Length 22;  
 Best Local Similarity 86.4%; Pred. No. 9e-08;  
 Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0.

OY 1 LLSWGCKGRGLVCYSYVQNNST 22  
 DB 1 LLSWGCKGRGLVCYSYVQNNST 22

RESULT 5  
 ID AAM07346 standard; peptide; 40 AA.  
 AC AAM07346;  
 DT 03-JUN-1997 (first entry)  
 DE Partial sequence of gp41 from HIV-1 gp. O strain BCF07 (MAN).  
 XX Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;  
 XX C233-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;  
 XX primer; hybridisation; amplification; PCR; polymerase chain reaction;  
 XX immunogen; antibody.  
 XX Human immunodeficiency virus type 1.  
 XX MO627013-A1.  
 XX 06-SEP-1996.  
 XX 26-FEB-1996; 96MO-FR00234.  
 XX 27-FEB-1995; 95FR-000236.  
 XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX Chalk-Baudier ML, Lousest-Ajaka I, Ly T, Saragosti S, Simon F;  
 XX WPI: 1996-412779/41.  
 XX N-PSDB; AAT44922.  
 XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
 XX antibodies - useful for diagnosis, screening and typing, or as  
 XX immunogens  
 XX Claim 12; Page 34; 71pp; French.  
 XX Human immunodeficiency virus type 1 (HIV-1) strains are currently

CC divided into 2 major groups based on the nucleotide sequences of the  
 CC envelop gene (env): group M containing sub-groups A-G, and group O  
 CC containing the strains AM70 and WPS180. The invention relates to the  
 CC discovery of several new strains of HIV-1 which can be placed in group O,  
 CC based on the partial sequences of the C233-env, gp41 and gag genes (see  
 CC AAT44907-39 and AAM07232-64). The novel strains have been deposited  
 CC (MAN), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence  
 CC presented here is from the strain BCF07 (MAN) and corresponds to a  
 CC fragment of the gp41 protein encoded by the env gene. The nucleic acids  
 CC can be used to detect gp. O HIV-1 strains by hybridisation or (as  
 CC primers) for the detection of gp. O HIV-1 strains by screening and typing of such  
 CC strains. Peptides encoded by the gp. O HIV-1 strains can be used as immunogens  
 CC to raise Ab for detecting gp. O HIV-1.

S0 Sequence 40 AA;  
 Query Match 89.8%; Score 114; DB 17; Length 40;  
 Best Local Similarity 86.4%; Pred. No. 4.4e-08;  
 Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0.

OY 1 LLSWGCKGRGLVCYSYVQNNST 22  
 DB 19 LLSWGCKGRGLVCYSYVQNNST 40

RESULT 6  
 ID AAM07352 standard; peptide; 40 AA.  
 AC AAM07352;  
 DT 03-JUN-1997 (first entry)  
 DE Partial sequence of gp41 from HIV-1 gp. O strain BCF13.  
 XX Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;  
 XX C233-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;  
 XX primer; hybridisation; amplification; PCR; polymerase chain reaction;  
 XX immunogen; antibody.  
 XX Human immunodeficiency virus type 1.  
 XX MO627013-A1.  
 XX 06-SEP-1996.  
 XX 26-FEB-1996; 96MO-FR00234.  
 XX 27-FEB-1995; 95FR-000236.  
 XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX Chalk-Baudier ML, Lousest-Ajaka I, Ly T, Saragosti S, Simon F;  
 XX WPI: 1996-412779/41.  
 XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
 XX antibodies - useful for diagnosis, screening and typing, or as  
 XX immunogens  
 XX Claim 12; Page 46; 71pp; French.  
 XX Human immunodeficiency virus type 1 (HIV-1) strains are currently  
 CC divided into 2 major groups based on the nucleotide sequences of the  
 CC envelop gene (env): group M containing sub-groups A-G, and group O  
 CC containing the strains AM70 and WPS180. The invention relates to the  
 CC discovery of several new strains of HIV-1 which can be placed in group O,  
 CC based on the partial sequences of the C233-env, gp41 and gag genes (see  
 CC AAT44907-39 and AAM07232-64). The novel strains have been deposited as  
 CC (MAN), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence

presented here is from the strain BCF13 and corresponds to a fragment of the gp120 protein encoded by the env gene. The nucleotide sequence was determined by direct sequencing of the PCR product. The sequence was then compared with the sequence of the gp120 protein of the strain BCF13 (as determined by gene amplification, also for screening and typing of such strains). Peptides encoded by the nucleic acids can be used as immunogens to raise Ab for detecting gp. O HIV-1.

Sequence 40 AA;

Query Match 88.4%; Score 112; DB 17; Length 40;

Best Local Similarity 86.4%; Pred. No. 8e-08; 2; Mismatches 0; Gaps 0;

Matches 19; Conservative 1; Indels 0; Gaps 0;

1 LLSGNGCKRLVCTYSVQNMST 22

11 LLSGNGCKRLVCTYSVQNMST 40

RESULT 7

AAW80469 standard; peptide; 32 AA.

AAW80469;

28-JUN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

MO9845323-A1.

15-OCT-1998.

06-APR-1998; 98MO-FR00691.

24-FEB-1998; 98FR-0002212.

09-APR-1997; 97FR-0004356.

(SNFI) PASTEUR SANOPI DIAGNOSTICS SA.

Chenboux DMB; Delagrange JFI; Gabelle SX; Rieunier FI;

WPI; 1998-561390/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by

human immune deficiency virus of group O

Claim 6; Page 44; 55pp; French.

AAW80469-74 represent synthetic peptides (either linear or cyclized by

Cys-Cys disulfide bonds). The peptides represent variable sequences

connected around short highly conserved sequences present in isolates

of group O human immune deficiency virus (HIV). The peptides are

useful as immunological reagents for detecting infection by group O

human immune deficiency virus (HIV).

Sequence 32 AA;

Query Match 87.4%; Score 111; DB 19; Length 32;

Best Local Similarity 81.8%; Pred. No. 8e-08; 2; Mismatches 0; Gaps 0;

Matches 18; Conservative 2; Indels 0; Gaps 0;

1 LLSGNGCKRLVCTYSVQNMST 22

11 LLSGNGCKRLVCTYSVQNMST 32

RESULT 8

AAW07351

ID AAW07351 standard; peptide; 41 AA.

AAW07351;

03-JUN-1997 (first entry)

Partial sequence of gp41 from HIV-1 gp. O strain BCF12.

Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;

C2V3-env; gp41; gp89; retrovirus; strain; gp120; hypervariable loop;

primers; hybridization; amplification; PCR; polymerase chain reaction;

immunogen; antibody.

Human immunodeficiency virus type 1.

MO9627013-A1.

06-SEP-1996.

26-FEB-1996; 96MO-FR00294.

27-FEB-1995; 95FR-0002236.

(ASST-) ASSOCIANCE PUBLIQUE HOSPITAL PARIS

(INRA) INSERM INST NAT SANTE & RECH MEDICALE.

Chaix-Baudier ML, Lousset-Ajaka I, Ly T, Sargueil S, Simon F;

WPI; 1996-412779/41.

New isolate of HIV-1 group O, related DNA fragments, peptide(s) and

antibodies - useful for diagnosis, screening and typing, or as

immunogens

Claim 12; Page 46; 71pp; French.

Human immunodeficiency virus type 1 (HIV-1) strains are currently

divided into 2 major groups based on the nucleotide sequence of the

env gene (env) and the gp120 protein (gp120) of the envelope. The

discovery of several new strains of HIV-1 which can be placed in group O,

based on the partial sequences of the C2V3-env, gp41 and gag genes (see

AAW4907-39 and AAW07329-64). The novel strains have been deposited as

retroviruses C2V3-1-1544 (BCP02 (BSH)), 1543 (BCP01 (PAN)), 1546 (BCP07

(MAN)), 1547 (BCP08 (RKO)) and 1548 (BCP03 (POC)) upon the sequence of

the gp120 protein encoded by the env gene. The nucleic acids can be used

to detect gp. O HIV-1 strains by hybridization or (as primers) by gene

amplification, also for screening and typing of such strains. Peptides

encoded by the nucleic acids can be used as immunogens to raise Ab for

detecting gp. O HIV-1.

Sequence 41 AA;

Query Match 87.4%; Score 111; DB 17; Length 41;

Best Local Similarity 81.8%; Pred. No. 1.1e-07; 2; Mismatches 0; Gaps 0;

Matches 18; Conservative 2; Indels 0; Gaps 0;

1 LLSGNGCKRLVCTYSVQNMST 22

11 LLSGNGCKRLVCTYSVQNMST 40

RESULT 9

AAV05565

AAV05565 standard; protein; 113 AA.

AAV05565;

19-JUL-1999 (first entry)

HIV-1 group O isolate MP539-FBWC gp41 antigen.

KW HIV-1 group O, Outlier strain; gp41, envelope protein; antigen;  
 KM vaccine; diagnosis; AIDS.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PH Key Location/Qualifiers  
 FT Misc-difference 65 /note="encoded by AMW"  
 FT Misc-difference 74 /note="encoded by ATR"  
 FT Misc-difference 84 /note="encoded by GAK"  
 FT Misc-difference 86 /note="encoded by AGV"  
 XX  
 XX MO9904011-A2.  
 XX  
 PD 28-JUN-1999.  
 XX  
 XX 20-JUL-1998; 98WO-EP04522.  
 XX  
 XX 18-JUL-1997; 97EP-0870110.  
 XX (INNO-) INNOGENETICS NV.  
 XX Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;  
 XX WPI: 1999-132255/11.  
 DR N-PSDB; AAY05565.  
 XX  
 XX New isolated HIV-1 group O strains - used to produce  
 PT polynucleotides, antigens and antibodies for use in diagnosis and in  
 FT vaccines for prevention of HIV-1 infection.  
 XX  
 PS Claim 3; Fig 6; 162pp; English.  
 XX  
 XX The present sequence is an antigen of the gp41 protein of HIV-1  
 CC group O (Outlier) strain MP539-PBM, a Cameroon isolate. The  
 CC antigen relates to new HIV-1 group O antigens (see AAY05546-623),  
 CC and nucleic acids encoding them (see  
 CC AA23154-80) in the diagnosis and  
 CC used as reagents for detecting HIV-1 group O infection and for  
 CC differentiating different types of HIV-1 group O infection.  
 CC Vaccines that provide protective immunity against HIV-1 infection, in  
 CC particular against HIV-1 group O infection, comprise at least one  
 CC HIV-1 type O antigen, a nucleic acid encoding such an antigen, a  
 CC virus-like particle comprising such an antigen, or an attenuated  
 CC HIV-1 group O strain. The invention also relates to new  
 CC HIV-1 group O strains, mostly from patients from Cameroon and its  
 CC neighbouring countries.  
 XX  
 SO Sequence 113 AA;  
 XX  
 Query Match 87.4%; Score 111; DB 20; Length 113;  
 ID AAY05625 Similarity 81.8%; Pred. No. 2,8e-07;  
 Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0.  
 XX  
 OY 1 LQSGCKGRRLVCYTSVOVNKT 22  
 DB 39 LAMWCKGRRLVCYTSVOVNKT 60  
 XX  
 XX  
 XX  
 XX AAY05625;  
 XX  
 XX 19-JUL-1999 (first entry)  
 XX  
 XX HIV-1 group O isolate M645 envelope protein (Env).  
 XX  
 XX HIV-1 group O; Outlier strain; envelope protein; Env; antigen;

KW vaccine; diagnosis; AIDS.  
 KM  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PH MO9904011-A2.  
 XX  
 PD 28-JUN-1999.  
 XX  
 XX 20-JUL-1998; 98WO-EP04522.  
 XX  
 XX 18-JUL-1997; 97EP-0870110.  
 XX (INNO-) INNOGENETICS NV.  
 XX Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;  
 XX WPI: 1999-132255/11.  
 DR N-PSDB; AA231580.  
 XX  
 XX New isolated HIV-1 group O strains - used to produce  
 PT polynucleotides, antigens and antibodies for use in diagnosis and in  
 FT vaccines for prevention of HIV-1 infection.  
 XX  
 PS Claim 3; Fig 8A; 162pp; English.  
 XX  
 XX The present sequence is a partial Env polypeptide of HIV-1 group O  
 CC (Outlier) strain MP539-PBM, a Cameroon isolate. The  
 CC antigen relates to new HIV-1 group O antigens (see AAY05546-623)  
 CC of M645 (see AA231580). The invention relates to new HIV-1 group O  
 CC antigens, especially envelope protein antigens (see AAY05546-623)  
 CC and the use of these antigens, or nucleic acids encoding them (see  
 CC AA23154-80), in the diagnosis and prophylaxis of AIDS. They can be  
 CC used as reagents for detecting HIV-1 group O infection and for  
 CC differentiating different types of HIV-1 group O infection.  
 CC Vaccines that provide protective immunity against HIV-1 infection, in  
 CC particular against HIV-1 group O infection, comprise at least one  
 CC HIV-1 type O antigen, a nucleic acid encoding such an antigen,  
 CC a virus-like particle comprising such an antigen, or an attenuated  
 CC form of an HIV-1 type O strain. The invention also relates to new  
 CC HIV-1 group O strains, obtained from patients from Cameroon, Gabon,  
 CC Tchad, Nigeria, Senegal and Niger.  
 XX  
 SO Sequence 715 AA;  
 XX  
 Query Match 87.4%; Score 111; DB 20; Length 715;  
 ID AAB12212 Similarity 86.4%; Pred. No. 1,6e-06;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 OY 1 LQSGCKGRRLVCYTSVOVNKT 22  
 DB 628 LAMWCKGRRLVCYTSVOVNKT 649  
 XX  
 XX  
 XX  
 XX AAB12212;  
 XX  
 XX 10-NOV-2000 (first entry)  
 XX  
 XX Partial sequence of HIV-1 strain BCF13 gp41 immunodominant region.  
 XX  
 XX HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;  
 KM acquired immunodeficiency syndrome; group O HIV; gp41; BCF13.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PH EPI013766-A2.  
 XX  
 XX 28-JUN-2000.  
 XX  
 XX 29-NOV-1999; 99EP-0309401.





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OY      1  LLSGCKGRIVCYTSVQVNST 22
DB      1  LLSGCKGRIVCYTSVQVNST 22

RESULT 14
AA012231 standard, peptide, 33 AA.
AC      AA012231;
DE      10-NOV-2000 (first entry)
XX
XX      Partial sequence of HIV-1 strain MAN gp41 immunodominant region.
DE      HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;
XX      acquired immunodeficiency syndrome; group O HIV; gp41; MAN.
XX
XX      Human immunodeficiency virus type 1.
XX      EPI013766-A2.
XX      28-JUN-2000.
XX      29-NOV-1999; 99EP-0103491.
XX      30-NOV-1998; 98US-0110292.
XX      08-FEB-1999; 99US-0119138.
XX      04-NOV-1999; 99US-0433428.
XX      (ORF1-) ORF10-CLINICAL DIAGNOSTICS INC.
XX      De Leyva R, Zheng J;
XX      WPI; 2000-402205/35.
XX      New antigenic peptides and peptide functional derivatives, useful for
XX      detection of antibodies produced in response to human immunodeficiency
XX      virus group O antibodies.
XX      Example 1; Fig 1; 52pp; English.
XX
XX      The present sequence is a partial gp41 protein of Human immunodeficiency
XX      virus type 1 (HIV-1) strain MAN. HIV is the principle aetiological
XX      agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV
XX      envelope protein, and may be used as an antigen for the detection of
XX      HIV antibodies produced in response to HIV infection. MAN is a member of
XX      HIV group O. The present sequence was used in a sequence homology alignment
XX      of gp41. This sequence was used in a sequence homology alignment of gp41
XX      which in turn was used to derive a consensus sequence peptide: peptide
XX      147 (AA012254).
XX
XX      Sequence 33 AA:
XX
XX      Query Match      85.8%; Score 109; DB 21; Length 33;
XX      Best local similarity 90.0%; Pred No. 1,6e-071;
XX      Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY      1  LLSGCKGRIVCYTSVQVNST 20
DB      14  LLSGCKGRIVCYTSVQVNST 33

RESULT 15
AA007343 standard, peptide; 40 AA.
AC      AA007343;
DE      03-JUN-1997 (first entry)
XX
XX      Partial sequence of gp41 from HIV-1 gp. O strain BCP02 (ESS).

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XX      Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;
XX      C23-Env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;
XX      immunogen; antigen; epitope; epitope; epitope; epitope; epitope; epitope;
XX      immunogen; antibody.
XX
XX      Human immunodeficiency virus type 1.
XX      W09627013-A1.
XX      06-SEP-1996.
XX      26-FEB-1996; 96MO-FR00294.
XX      27-FEB-1995; 95FR-0002236.
XX      (AISI-) ASSISTANCE PUBLIQUE HOPITALUX PARIS.
XX      (ITER-) INSERM INST NAT SANTE & RECH MEDICALE.
XX      Chakr-Baudier ML, Lousseer-AJala I, Ly T, Saragosti S, Simon F;
XX      WPI; 1996-412779/41.
XX      N-PSDB; AA744918.
XX      New strains of HIV-1 group O, related DNA fragments, peptide(s) and
XX      antibodies - useful for diagnosis, screening and typing, or as
XX      immunogens
XX      Claim 12; Page 33; 71pp; French.
XX
XX      Human immunodeficiency virus type 1 (HIV-1) strains are currently
XX      divided into 2 major groups based on the nucleotide sequences of the
XX      env gene (env): group M containing sub-groups A-G, and group O
XX      containing sub-groups A-G and O. The present invention relates to the
XX      discovery of new strains of HIV-1, which are related to group O
XX      based on the partial sequences of the C23-Env, gp41 and gag genes (see
XX      AAT44907-39 and AA007328-64). The novel strains have been deposited as:
XX      retroviruses CCMC I-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07
XX      (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence
XX      presented here is from the strain BCP02 (ESS) and corresponds to a
XX      fragment of the gp41 protein encoded by the env gene. The nucleic acids
XX      and the peptides encoded by the gp41 protein are useful for the diagnosis of
XX      primary or secondary HIV infection, as well as for the identification of
XX      strains. Peptides encoded by the nucleic acids can be used as immunogens
XX      to raise Ab for detecting gp. O HIV-1.
XX
XX      Sequence 40 AA:
XX
XX      Query Match      85.8%; Score 109; DB 17; Length 40;
XX      Best local similarity 90.0%; Pred No. 1,2e-077;
XX      Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY      1  LLSGCKGRIVCYTSVQVNST 22
DB      19  LLSGCKGRIVCYTSVQVNST 40

Search completed: May 29, 2003, 10:36:21
Job time : 29.333 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:36 / Search time 9.95238 Seconds

Title: US-09-147-362a-5 (without alignment)  
65,040 Million cell updates/sec

Sequence: 1 LLOSWGCKRLVCTVGMNST 22

Perfect score: 127

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 2942292 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter: 45 summaries

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Issued Patents AA:  
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3: /cgn2\_6/pdata/1/1aa/6a COMB pep.\*  
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5: /cgn2\_6/pdata/1/1aa/6c COMB pep.\*  
6: /cgn2\_6/pdata/1/1aa/6d COMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89.8	40	3	US-08-694-699-39	Sequence 39, Appl
2	89.8	40	3	US-08-694-699-39	Sequence 39, Appl
3	88.2	40	3	US-08-694-699-39	Sequence 39, Appl
4	88.2	40	3	US-08-694-699-39	Sequence 39, Appl
5	88.2	40	3	US-08-694-699-39	Sequence 39, Appl
6	87.4	41	3	US-08-694-699-39	Sequence 39, Appl
7	87.4	41	3	US-08-694-699-39	Sequence 39, Appl
8	86.6	41	3	US-08-694-699-39	Sequence 39, Appl
9	85.8	40	3	US-08-694-699-39	Sequence 39, Appl
10	85.8	40	3	US-08-694-699-39	Sequence 39, Appl
11	85.8	40	3	US-08-694-699-39	Sequence 39, Appl
12	85.8	40	3	US-08-694-699-39	Sequence 39, Appl
13	85.8	40	3	US-08-694-699-39	Sequence 39, Appl
14	85.8	40	3	US-08-694-699-39	Sequence 39, Appl
15	84.3	41	3	US-08-694-699-39	Sequence 39, Appl
16	84.3	41	3	US-08-694-699-39	Sequence 39, Appl
17	84.3	41	3	US-08-694-699-39	Sequence 39, Appl
18	84.3	41	3	US-08-694-699-39	Sequence 39, Appl
19	84.3	41	3	US-08-694-699-39	Sequence 39, Appl
20	84.3	41	3	US-08-694-699-39	Sequence 39, Appl
21	84.3	41	3	US-08-694-699-39	Sequence 39, Appl
22	84.3	41	3	US-08-694-699-39	Sequence 39, Appl
23	84.3	41	3	US-08-694-699-39	Sequence 39, Appl
24	84.3	41	3	US-08-694-699-39	Sequence 39, Appl
25	84.3	41	3	US-08-694-699-39	Sequence 39, Appl
26	84.3	41	3	US-08-694-699-39	Sequence 39, Appl
27	81.9	40	3	US-08-694-699-39	Sequence 39, Appl

28	104	81.9	40	3	US-08-694-699-39	Sequence 42, Appl
29	104	81.9	40	3	US-08-694-699-39	Sequence 42, Appl
30	104	81.9	40	3	US-08-694-699-39	Sequence 42, Appl
31	104	81.9	40	3	US-08-694-699-39	Sequence 42, Appl
32	104	81.9	40	3	US-08-694-699-39	Sequence 42, Appl
33	104	81.9	40	3	US-08-694-699-39	Sequence 42, Appl
34	104	81.9	40	3	US-08-694-699-39	Sequence 42, Appl
35	103	81.1	33	4	US-09-433-428D-7	Sequence 7, Appl
36	103	81.1	33	4	US-09-433-428D-7	Sequence 7, Appl
37	103	81.1	33	4	US-09-433-428D-7	Sequence 7, Appl
38	103	81.1	33	4	US-09-433-428D-7	Sequence 7, Appl
39	103	81.1	33	4	US-09-433-428D-7	Sequence 7, Appl
40	102	80.3	33	4	US-09-433-428D-7	Sequence 7, Appl
41	102	80.3	33	4	US-09-433-428D-7	Sequence 7, Appl
42	101	79.5	33	4	US-09-433-428D-7	Sequence 7, Appl
43	101	79.5	33	4	US-09-433-428D-7	Sequence 7, Appl
44	101	79.5	33	4	US-09-433-428D-7	Sequence 7, Appl
45	101	79.5	33	4	US-09-433-428D-7	Sequence 7, Appl

## ALIGNMENTS

RESULT 1  
US-08-694-699-39  
Sequence 39, Application US/08934699  
GENERAL INFORMATION:  
APPLICANT: SARACOSTI, SIMON  
APPLICANT: LOUISBERT-ALMA, IBITISSAM  
APPLICANT: LY, THOM-DONG  
APPLICANT: CHAI-X-BANDIER, MARIE-LAURE  
TITLE OF INVENTION: VITROUS, AND USES THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSER: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
FLOOR  
ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION Database #1.0, Version #1.30  
APPLICATION NUMBER: US/08/694,699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA: PR 95/02236  
APPLICATION NUMBER: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
COMPLETENESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-08-894-699-39  
Query Match 89.8%; Score 114; DB 3; Length 40;  
Best Local Similarity 86.4%; Pred. No. 4.7e-10;  
Matches 19; Conservative 1; Mismatches 2; Indels 0;  
Caps 0;  
DB 19 LINSWCKGRKRLVCTSYVMNET 40

1 LINSWCKGRKRLVCTSYVMNET 22  
|||||  
DB 19 LINSWCKGRKRLVCTSYVMNET 40

RESULT 2  
US-09-444-410-39  
US-08-894-699-39  
Sequence 68; Application US/09444410  
Patent No. 6276975  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOB  
APPLICANT: LOUSSEST-AJAKA, IBITISSAM  
APPLICANT: LY, THOI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSER: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/444, 410  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/894, 699  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F., 614  
REGISTRATION/DOCKET NUMBER: 0354-0020-0PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEO ID NO: 39;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STANDARDS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-444-410-39

Query Match 89.8%; Score 114; DB 4; Length 40;  
Best Local Similarity 86.4%; Pred. No. 4.7e-10;  
Matches 19; Conservative 1; Mismatches 2; Indels 0;  
Caps 0;  
DB 19 LINSWCKGRKRLVCTSYVMNET 40

1 LINSWCKGRKRLVCTSYVMNET 22  
|||||  
DB 19 LINSWCKGRKRLVCTSYVMNET 40

RESULT 3  
US-08-894-699-68  
Sequence 68; Application US/08894699  
Patent No. 6030769  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOB  
APPLICANT: LOUSSEST-AJAKA, IBITISSAM  
APPLICANT: LY, THOI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSER: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/894, 699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F., 614  
REGISTRATION/DOCKET NUMBER: 0354-0020-0PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEO ID NO: 68;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STANDARDS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-68

Query Match 88.2%; Score 112; DB 3; Length 40;  
Best Local Similarity 86.4%; Pred. No. 9.2e-10;  
Matches 19; Conservative 1; Mismatches 2; Indels 0;  
Caps 0;  
DB 19 LINSWCKGRKRLVCTSYVMNET 40

1 LINSWCKGRKRLVCTSYVMNET 22  
|||||  
DB 19 LINSWCKGRKRLVCTSYVMNET 40

RESULT 4  
US-09-444-410-68  
Sequence 68; Application US/09444410  
Patent No. 6276975  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOB  
APPLICANT: LOUSSEST-AJAKA, IBITISSAM  
APPLICANT: LY, THOI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

```

1 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
2 TITLE OF INVENTION: VIRUSES, AND USES THEREOF
3 NUMBER OF SEQUENCES: 41
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
6 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
7 CITY: ARLINGTON
8 STATE: VA
9 COUNTRY: USA
10
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Floppy disk
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: PatentIn Release #1.0, Version #1.30
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/09/444,410
17 FILING DATE:
18 CLASSIFICATION:
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 08/894,699
21 FILING DATE:
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: FR 95/02236
24 FILING DATE: 27-FEB-1995
25 ATTORNEY/AGENT INFORMATION:
26 NAME: OBLON, NORMAN F.
27 REGISTRATION NUMBER: 24,614
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 703-413-3000
30 TELEFAX: 703-413-3000
31 INFORMATION FOR SEO ID NO: 68:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 40 amino acids
34 TYPE: amino acid
35 STRANDNESS: single
36 TOPOLOGY: linear
37 MOLECULE TYPE: peptide
38 US-09-444-410-68
39
40 Query Match 88.2%; Score 112; DB 4; Length 40;
41 Best Local Similarity 86.4%; Pred. No. 9.2e-10;
42 Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
43
44 1 LLSMGCKGRJVCYTSVQVNST 22
45 19 LLSMGCKGRJVCYTSVQVNST 40
46
47 RESULT 5
48 US-08-894-699-67
49 Sequence 67, Application US/08894699
50 Patent No. 6030789
51 APPLICANT: SIMON, FRANCOIS
52 APPLICANT: SARAGOSTI, SENIOR
53 APPLICANT: LOUSSERT-AJAKA, IBITISSAM
54 APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
55 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
56 TITLE OF INVENTION: VIRUSES, AND USES THEREOF
57 NUMBER OF SEQUENCES: 81
58 CORRESPONDENCE ADDRESS:
59 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
60 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
61 CITY: ARLINGTON
62 STATE: VA
63 COUNTRY: USA

```

```

1 ZIP: 22202
2 COMPUTER READABLE FORM:
3 MEDIUM TYPE: Floppy disk
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: PatentIn Release #1.0, Version #1.30
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/08/894,699
8 FILING DATE: 01-DEC-1997
9 CLASSIFICATION:
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: SCT/FR96/00294
12 FILING DATE: 26-FEB-1996
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: FR 95/02236
15 FILING DATE: 27-FEB-1995
16 ATTORNEY/AGENT INFORMATION:
17 NAME: OBLON, NORMAN F.
18 REGISTRATION NUMBER: 24,614
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: 703-413-3000
21 TELEFAX: 703-413-3000
22 INFORMATION FOR SEO ID NO: 67:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 41 amino acids
25 TYPE: amino acid
26 STRANDNESS: single
27 TOPOLOGY: linear
28 MOLECULE TYPE: peptide
29 US-08-894-699-67
30
31 Query Match 87.4%; Score 111; DB 3; Length 41;
32 Best Local Similarity 81.8%; Pred. No. 3.3e-09;
33 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
34
35 1 LLSMGCKGRJVCYTSVQVNST 22
36 19 LLSMGCKGRJVCYTSVQVNST 40
37
38 RESULT 6
39 US-09-444-410-67
40 Sequence 67, Application US/09444410
41 Patent No. 6270975
42 GENERAL INFORMATION:
43 APPLICANT: SIMON, FRANCOIS
44 APPLICANT: SARAGOSTI, SENIOR
45 APPLICANT: LOUSSERT-AJAKA, IBITISSAM
46 APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
47 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
48 TITLE OF INVENTION: VIRUSES, AND USES THEREOF
49 NUMBER OF SEQUENCES: 81
50 CORRESPONDENCE ADDRESS:
51 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
52 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
53 CITY: ARLINGTON
54 STATE: VA
55 COUNTRY: USA
56 ZIP: 22202
57 COMPUTER READABLE FORM:
58 MEDIUM TYPE: Floppy disk
59 OPERATING SYSTEM: IBM PC compatible
60 SOFTWARE: PatentIn Release #1.0, Version #1.30
61 CURRENT APPLICATION DATA:
62 APPLICATION NUMBER: US/09/444,410
63 FILING DATE:
64 CLASSIFICATION:
65 PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: 08/894,699  
FILING DATE: 27-FEB-1995  
PRIORITY APPLICATION DATA: FR 95/02236  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F., 614  
REFERENCE/DOCKET NUMBER: 0154-0020-OPCT  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
TYPE: amino acids  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
9-444-410-67

Query Match 87.4%; Score 111; DB 4; Length 41;  
Best Local Similarity 81.8%; Pred. No. 1,3e-09;  
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 LMSGCKRRLVCYTSVNMST 22  
DB 19 LMSGCKRRLVCYTSVNMST 40

RESULT 7  
US-09-433-4280-6  
Sequence 6, Application US/094334280  
Patent No. 6145910  
GENERAL INFORMATION:  
APPLICANT: Zheng, Jian  
INVENTOR: Zheng, Jian  
FILE REFERENCE: US-207-154,688  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO: 6  
TYPE: PRT  
STRANDNESS: single  
TOPOLOGY: linear  
ORGANISM: Human immunodeficiency virus type 1  
9-433-4280-6

Query Match 86.6%; Score 110; DB 4; Length 33;  
Best Local Similarity 90.0%; Pred. No. 1,5e-09;  
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 LMSGCKRRLVCYTSVNM 20  
DB 14 LMSGCKRRLVCYTSVNM 33

RESULT 8  
US-09-433-4280-25  
Sequence 25, Application US/094334280  
Patent No. 6145910  
GENERAL INFORMATION:  
APPLICANT: De Lays, Robert J.  
INVENTOR: Zheng, Jian  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
REFERENCE/DOCKET NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO: 25  
LENGTH: 33

TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-4280-25

Query Match 85.8%; Score 109; DB 4; Length 33;  
Best Local Similarity 90.0%; Pred. No. 2,1e-09;  
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 LMSGCKRRLVCYTSVNM 20  
DB 14 LMSGCKRRLVCYTSVNM 33

RESULT 9  
US-08-894-699-36  
Sequence 36, Application US/08894699  
Patent No. 620769  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARACOSTI, SENTOB  
APPLICANT: LOUISBERT-AJAKA, IBITISSAM  
APPLICANT: LY, THOM-DONG  
APPLICANT: CHAI-BANDIER, MARIE-LAURE  
INVENTOR: CHAI-BANDIER, MARIE-LAURE  
TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
SOFTWARE: Patent Ver. 2.0  
CURRENT APPLICATION DATA: Version #1.30  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997

CLASSIFICATION:  
PRIOR APPLICATION: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F., 614  
REFERENCE/DOCKET NUMBER: 0154-0020-OPCT  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-36

Query Match 85.8%; Score 109; DB 3; Length 40;  
Best Local Similarity 91.8%; Pred. No. 2,5e-09;  
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 LMSGCKRRLVCYTSVNMST 22  
DB 19 LMSGCKRRLVCYTSVNMST 40

RESULT 10  
US-08-894-699-37 Application US/08894699  
Patent No. 6010769  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SERGIO  
APPLICANT: LOUSSERT-AMANA, IBTISSEM  
APPLICANT: LY, THOI-DUONG MAIE-LAINE  
APPLICANT: CHAIX-BANDIER, MAIE-LAINE  
TITLE OF INVENTION: VIRUSES, AND USBS THEREOF  
TITLE OF INVENTION: VIRUSES, AND USBS THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: P.C.  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894, 699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION: DATA  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELEPHONE: 703-413-2220  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-37  
Query Match 85.8%; Score 109; DB 3; Length 40;  
Best Local Similarity 81.8%; Pred. No. 2.5e-09;  
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
DB 19 LINSNGCKRGLVCTSVNMNST 22  
1 LLSNGCKRGLVCTSVNMNST 22  
RESULT 11  
US-09-444-410-36  
Sequence 36, Application US/09444410  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SERGIO  
APPLICANT: LOUSSERT-AMANA, IBTISSEM  
APPLICANT: LY, THOI-DUONG MAIE-LAINE  
APPLICANT: CHAIX-BANDIER, MAIE-LAINE  
TITLE OF INVENTION: VIRUSES, AND USBS THEREOF  
TITLE OF INVENTION: VIRUSES, AND USBS THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: P.C.  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/444,410  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/894, 699  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELEPHONE: 703-413-2220  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-444-410-36  
Query Match 85.8%; Score 109; DB 4; Length 40;  
Best Local Similarity 81.8%; Pred. No. 2.5e-09;  
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
DB 19 LINSNGCKRGLVCTSVNMNST 22  
1 LLSNGCKRGLVCTSVNMNST 22

APPLICANT: CHAIX-BANDIER, MAIE-LAINE  
TITLE OF INVENTION: VIRUSES, AND USBS THEREOF  
TITLE OF INVENTION: VIRUSES, AND USBS THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: P.C.  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/444,410  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/894, 699  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELEPHONE: 703-413-2220  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-444-410-36  
Query Match 85.8%; Score 109; DB 4; Length 40;  
Best Local Similarity 81.8%; Pred. No. 2.5e-09;  
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
DB 19 LINSNGCKRGLVCTSVNMNST 22  
1 LLSNGCKRGLVCTSVNMNST 22  
RESULT 12  
US-09-444-410-37  
Sequence 37, Application US/09444410  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SERGIO  
APPLICANT: LOUSSERT-AMANA, IBTISSEM  
APPLICANT: LY, THOI-DUONG MAIE-LAINE  
APPLICANT: CHAIX-BANDIER, MAIE-LAINE  
TITLE OF INVENTION: VIRUSES, AND USBS THEREOF  
TITLE OF INVENTION: VIRUSES, AND USBS THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: P.C.  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/444,410  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/894, 699  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELEPHONE: 703-413-2220  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-444-410-36  
Query Match 85.8%; Score 109; DB 4; Length 40;  
Best Local Similarity 81.8%; Pred. No. 2.5e-09;  
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
DB 19 LINSNGCKRGLVCTSVNMNST 22  
1 LLSNGCKRGLVCTSVNMNST 22

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? COUNTRY: USA
? ZIP: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: RELEASE #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/444,410
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? PRIORITY NUMBER: 08/894,699
? FILING DATE:
? APPLICATION NUMBER: FR 95/02236
? FILING DATE: 27-FEB-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: OBLON, NORMAN F.
? REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 703-413-3000
? TELEFAX: 703-413-2220
? INFORMATION FOR SEQ ID NO: 37:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 40 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-09-444-410-37

Query Match 85.84; Score 109; DB 4; Length 40;
Base Local Similarity 85.84; Pred. No. 2, 5e-09;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCKGRVLCYTSVKNMST 22
DB 19 LLSWGCKGRVLCYTSVKNMST 40

RESULT 13
US-08-894-699-69
? Sequence 69, Application US/08894699
? Patent No. 6030769
? GENERAL INFORMATION:
? APPLICANT: SIMON, FRANCOIS
? APPLICANT: SPROOST, STEPHEN
? APPLICANT: LOUSBERT-ALAKA, IBITISSAM
? APPLICANT: LY, THOI-DUONG
? APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
? TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
? TITLE OF INVENTION: VIRUSES, AND USBS THEREOF
? NUMBER OF SEQUENCES: 81
? CORRESPONDENCE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
? ADDRESSEE: P.C.
? STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
? STREET: FLOOR
? CITY: ARLINGTON
? STATE: VA
? COUNTRY: USA
? ZIP: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/894,699
? FILING DATE: 01-DEC-1997
? CLASSIFICATION:

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? PRIOR APPLICATION DATA:
? PRIORITY NUMBER: GCT/FR96/00294
? FILING DATE: 26-FEB-1996
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: FR 95/02236
? FILING DATE: 27-FEB-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: OBLON, NORMAN F.
? REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 703-413-3000
? TELEFAX: 703-413-2220
? INFORMATION FOR SEQ ID NO: 69:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 40 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-08-894-699-69

Query Match 85.84; Score 109; DB 3; Length 41;
Base Local Similarity 85.84; Pred. No. 2, 2e-09;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCKGRVLCYTSVKNMST 22
DB 19 LLSWGCKGRVLCYTSVKNMST 40

RESULT 14
US-09-444-410-69
? Sequence 69, Application US/09444410
? Patent No. 6270975
? GENERAL INFORMATION:
? APPLICANT: SIMON, FRANCOIS
? APPLICANT: SPROOST, STEPHEN
? APPLICANT: LOUSBERT-ALAKA, IBITISSAM
? APPLICANT: LY, THOI-DUONG
? APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
? TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
? TITLE OF INVENTION: VIRUSES, AND USBS THEREOF
? NUMBER OF SEQUENCES: 81
? CORRESPONDENCE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
? ADDRESSEE: P.C.
? STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
? STREET: FLOOR
? CITY: ARLINGTON
? STATE: VA
? COUNTRY: USA
? ZIP: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/444,410
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? PRIORITY NUMBER: 08/894,699
? FILING DATE:
? APPLICATION NUMBER: FR 95/02236
? FILING DATE: 27-FEB-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: OBLON, NORMAN F.
? REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
? TELECOMMUNICATION INFORMATION:

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TELEPHONE: 703-413-3000  
TELEFAX: 703-413-3220  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
ORIENTATION: linear  
MOLWT: 10000  
US-09-444-410-69

Query Match 85.8%; Score 109; DB 4; Length 41;  
Best Local Similarity 81.8%; Pred. No. 2.6e-09;

Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWGCKGRIVCTYSVQNNST 22  
DB 19 LLSWGCKGRIVCTYSVQNNST 40

BLT 15.  
US-09-433-428D-30  
Sequence 30; Application US/09433428D  
GENERAL INFORMATION:  
APPLICANT: De Leys, Robert J.  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
INVENTOR: SEQ ID NOS: 70  
SOFTWARE: Protein ver. 2.0  
SEQ ID NO 30  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-30

Query Match 84.3%; Score 107; DB 4; Length 33;  
Best Local Similarity 85.0%; Pred. No. 4e-09;

Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 LLSWGCKGRIVCTYSVQNN 20  
DB 14 LLSWGCKGRIVCTYSVQNN 33

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time: 10.9524 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:39:21 ; Search time 19.0317 Seconds

(without alignments)  
117,011 Million cell updates/sec

Title: US-09-147-362a-5

Perfect score: 127

Sequence: 1 LLAGMCGKGRIVCTYSVQNNST 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 383519 seqs, 101223694 residues

1 number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :	Published Applications ANI *
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2: /cgn2_6/p/odata/2/pubpa/PCT_NEW_PUB pep.*	
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13: /cgn2_6/p/odata/2/pubpa/US60_PUBCOMB pep.*	
14: /cgn2_6/p/odata/2/pubpa/US60_PUBCOMB pep.*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score of the result being printed, and is derived by analysis of the local score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	107	84.3	215	1 US-08-911-824-58	Sequence 58, App1
2	107	84.3	245	1 US-08-911-824-48	Sequence 48, App1
3	107	84.3	245	1 US-08-911-824-48	Sequence 52, App1
4	107	84.3	245	1 US-08-911-824-48	Sequence 56, App1
5	107	84.3	460	1 US-08-911-824-60	Sequence 60, App1
6	107	84.3	468	1 US-08-911-824-60	Sequence 95, App1
7	107	84.3	490	1 US-08-911-824-50	Sequence 50, App1
8	107	84.3	526	1 US-08-911-824-97	Sequence 97, App1
9	107	84.3	618	1 US-08-911-824-54	Sequence 54, App1
10	107	84.3	706	1 US-08-911-824-51	Sequence 93, App1
11	107	84.3	706	1 US-08-911-824-51	Sequence 91, App1
12	107	84.3	873	1 US-08-911-824-81	Sequence 81, App1
13	107	84.3	873	1 US-08-911-824-81	Sequence 86, App1
14	104	81.9	200	10 US-09-854-816-104	Sequence 104, App1
15	104	81.9	35	9 US-10-026-741-101	Sequence 7, App1
16	101	79.5	37	9 US-10-026-741-7	Sequence 90, App1
17	101	79.5	37	9 US-10-026-741-90	Sequence 47, App1
18	101	79.5	37	9 US-10-026-741-4	Sequence 102, App1
19	101	79.5	37	9 US-10-026-741-102	

20	100	78.7	37	9 US-10-026-741-94	Sequence 94, App1
21	100	78.7	104	9 US-10-026-741-100	Sequence 100, App1
22	100	78.7	35	9 US-09-886-156-82	Sequence 62, App1
23	97	76.4	35	9 US-09-886-156-82	Sequence 62, App1
24	97	76.4	35	9 US-09-886-156-82	Sequence 62, App1
25	97	76.4	35	9 US-09-886-156-82	Sequence 62, App1
26	97	76.4	35	9 US-09-886-156-82	Sequence 62, App1
27	97	76.4	35	9 US-09-886-156-82	Sequence 62, App1
28	97	76.4	146	12 US-10-000-321-105	Sequence 105, App1
29	97	76.4	204	10 US-09-854-816-103	Sequence 103, App1
30	97	76.4	23	12 US-10-000-321-105	Sequence 105, App1
31	97	76.4	23	12 US-10-000-321-105	Sequence 105, App1
32	97	76.4	23	12 US-10-000-321-105	Sequence 105, App1
33	97	76.4	23	12 US-10-000-321-105	Sequence 105, App1
34	96	75.6	213	10 US-09-854-816-103	Sequence 103, App1
35	95	74.8	23	12 US-10-000-321-105	Sequence 105, App1
36	95	74.8	23	12 US-10-000-321-105	Sequence 105, App1
37	95	74.8	23	12 US-10-000-321-105	Sequence 105, App1
38	95	74.8	23	12 US-10-000-321-105	Sequence 105, App1
39	94	74.8	23	12 US-10-000-321-105	Sequence 105, App1
40	94	74.8	23	12 US-10-000-321-105	Sequence 105, App1
41	83	65.4	37	9 US-10-026-741-84	Sequence 84, App1
42	83	65.4	198	10 US-09-854-816-77	Sequence 77, App1
43	83	65.4	198	10 US-09-854-816-78	Sequence 78, App1
44	83	65.4	198	10 US-09-854-816-80	Sequence 80, App1
45	83	65.4	198	10 US-09-854-816-89	Sequence 89, App1

## ALIGNMENTS

RESULT 1  
US-08-911-824-58  
Sequence 58, Application US/08911824  
Published ID NO US2003000432A1  
GENERAL INFORMATION  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Yamauchi, Julie  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Golden, Alan M.  
APPLICANT: Devere, Shelli K.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV  
FILE REFERENCE: 6165.US.01  
CURRENT APPLICATION NUMBER: US/08/911,824  
CURRENT FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 121  
SEQ ID NOS: 58  
SEQ ID NOS: 58  
LENGTH: 215  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: Encodes recombinant protein pCO-8PL  
US-08-911-824-58  
Query Match 84.3%; Pred 107, DB 1; Length 215;  
Best Local Similarity 77.3%; Score No. 5, 76-08;  
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Db 127 LLAGMCGKGRIVCTYSVQNNST 148  
OY 1 LLAGMCGKGRIVCTYSVQNNST 22  
RESULT 2  
US-08-911-824-48  
Sequence 48, Application US/08911824  
Published ID NO US2003000432A1  
GENERAL INFORMATION  
APPLICANT: Abbott Laboratories



```

APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US.O1
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 95
LENGTH: 488
TYPE: PRF
ORGANISM: Human Immunodeficiency Virus
OTHER INFORMATION: Encodes recombinant protein pCO-14PL
US-08-911-824-95

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Query Match      84.3% Score 107; DB 1; Length 488;
Best Local Similarity 77.3%; Pred.No.1,2e-07;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1  LLSWGCKGRLLVCTSYVKNST 22
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127 LLLMGGCKRRLICITSYVKNST 148

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RESULT 7
US-08-911-824-50
Sequence 50; Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US.O1
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 50
LENGTH: 490
TYPE: PRF
ORGANISM: Human Immunodeficiency Virus
OTHER INFORMATION: Encodes recombinant protein pCO-9CKS
US-08-911-824-50

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```

Query Match      84.3% Score 107; DB 1; Length 490;
Best Local Similarity 77.3%; Pred.No.1,2e-07;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1  LLSWGCKGRLLVCTSYVKNST 22
|||
372 LLLMGGCKRRLICITSYVKNST 393

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RESULT 8
US-08-911-824-97
Sequence 97; Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.

```

```

APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US.O1
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 526
LENGTH: 526
TYPE: PRF
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-15CKS
US-08-911-824-97

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```

Query Match      84.3% Score 107; DB 1; Length 526;
Best Local Similarity 77.3%; Pred.No.1,2e-07;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1  LLSWGCKGRLLVCTSYVKNST 22
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372 LLLMGGCKRRLICITSYVKNST 393

```

```

RESULT 9
US-08-911-824-54
Sequence 54; Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US.O1
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 54
LENGTH: 618
TYPE: PRF
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-11CKS
US-08-911-824-54

```

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Query Match      84.3% Score 107; DB 1; Length 618;
Best Local Similarity 77.3%; Pred.No.1,2e-07;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1  LLSWGCKGRLLVCTSYVKNST 22
|||
372 LLLMGGCKRRLICITSYVKNST 393

```

```

RESULT 10
US-08-911-824-93
Sequence 93; Application US/08911824
Publication No. US20030004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.

```

APPLICANT: Devate, Shihli G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
DIAGNOSIS AND TREATMENT OF HIV-1 INFECTION  
FILE REFERENCE NUMBER: 6145 US OI  
CURRENT APPLICATION NUMBER: US/08/911,824  
CURRENT FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 61  
LENGTH: 873  
ORIGIN: GenBank  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: HIV-1 Group O Isolate HAM112  
US-08-911-824-61

Query Match      84.3% Score 107, DB 1, Length 873;  
Best Local Similarity    77.3%; Fred. No. 2.3e-07;  
Matches         17 Conservative    2; Mismatches    3; Indels    0; Gaps    0.

Db                  601 LILNMCKCKRLCYTSVKMNET 622

QY                  1 LLSGCKCKSLVCTSVCMST 22  
| | | | | | | | | | | | | | | | | | | | | |  
| | | | | | | | | | | | | | | | | | | | | |

RESULT 13  
USID: 0025-743-06  
Sequence 86, Application US/10026741  
Publication No.: US20030049604A1  
GENERAL INFORMATION:  
APPLICANT: CHARNEAU, PIERRE  
          CIVIEL, FRANCOISE  
          BORRANI, ANDREW  
          D'AMICO, JOSEPHINE  
          CHERTAD, DENISE  
          MONTAGNIER, LUC  
          DONON DE SAINT-MARTIN, JACQUELINE  
COHEN, JACQUES  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (GR  
SUBTYPE) ANTIGENS  
NUMBER OF SEQUENCES: 103  
CORRESPONDING ADDRESSES: Anderson Henderson, Farabow, Garrett &  
                          Dunner, L.L.P.  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER: IBM PC compatible  
MEDICAL TYPE: PLASMA  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/026,741  
FILING DATE: 27-Dec-2001  
PRIORITY: NONE  
PRIOR APPLICATION NUMBER: US 08/817,441  
FILING DATE: 31-AUG-1998  
APPLICATION NUMBER: PCT/FR 95/01391  
FILING DATE: 20-OCT-1995  
APPLICATION NUMBER: FR 9413554  
FILING DATE: 20-OCT-1994  
APPLICATION NUMBER: FR 9502526  
PUBLICATION NUMBER: EP 06145-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03260, 6005-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
FAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 86:  
US-10-026-741-06

Query Match 81.9% Score 104; DB 9; Length 37;  
Best Local Similarity 77.3%; Pred. No. 2, 9e-07;  
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

DB 1 L10SGCKGRVLCYTSVYKNT 22  
14 L10SGCKGRVLCYTSVYKNT 35

RESULT 14  
Sequence 104, Application US/09854816  
Patent No. US0002015173A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braised  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasiluk  
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
ZIP: 94020

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinProtin (Genentech)  
CURRENT APPLICATION DATA: US/09/854, 816  
FILING DATE: 15-MAR-2000  
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
REGISTRATION NUMBER: 31000000  
REFERENCE/DOCKET NUMBER: P1005R2  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 200  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 104:

US-09-854-816-104  
Query Match 81.9% Score 104; DB 10; Length 200;  
Best Local Similarity 77.3%; Pred. No. 1, 4e-07;  
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

DB 1 L10SGCKGRVLCYTSVYKNT 22  
1 L10SGCKGRVLCYTSVYKNT 22

DB 126 L10SGCKGRVLCYTSVYKNT 147

RESULT 15  
US-10-026-741-101  
Sequence 101, Application US/10026741  
Publication No. US20030049604A1  
GENERAL INFORMATION:  
APPLICANT: CHARNEAU, PIERRE  
CLAVEL, FRANCOISE  
BOMMAN, ANDREW  
MONTAGNIER, DANIEL  
MONTAGNIER, LUC  
DONJON DE SAINT-MARTIN, JACQUELINE  
COHEN, JACQUES

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Finmeag, Henderson, Farbow, Garrett &  
Dunnet, L.L.P.  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-2015

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/10/026, 741  
FILING DATE: 31-AUG-1998  
PRIORITY APPLICATION DATA: C-2001  
APPLICATION NUMBER: US 08/817,441  
FILING DATE: 31-AUG-1998  
APPLICATION NUMBER: PCT/FR 95/01391  
FILING DATE: 20-OCT-1995  
APPLICATION NUMBER: FR 9412554  
FILING DATE: 20-OCT-1995  
APPLICATION NUMBER: FR 95052526  
FILING DATE: 03-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03260, 6005-00000  
TELEPHONE: 202-462-0800  
TELEFAX: 202-462-0800  
INFORMATION FOR SEQ ID NO: 101:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 101:  
US-10-026-741-101

Query Match 79.5% Score 101; DB 9; Length 35;  
Best Local Similarity 72.7%; Pred. No. 7, 4e-08;  
Matches 16; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

DB 1 L10SGCKGRVLCYTSVYKNT 22  
14 L10SGCKGRVLCYTSVYKNT 35

Search completed: May 29, 2003, 11:03:57  
Job time: 15:03:17 secs

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Matches 16; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 Oy 1 LLSGCGKGRILCTTVQNMST 22  
 |||||:|||||:|||||:  
 Db 607 LNLWGCGKGRILCTTVQNMST 628

RESULT 3  
 552330 env polyprotein - human immunodeficiency virus type 1 (fragment)  
 A:Accession: S22002  
 C:Date: 06-Jun-1995 #sequence\_revision 21-Jul-1995 #text\_change 26-Aug-1999  
 C:Entry: 552330  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, January 1995  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by HIV-1 RNA  
 A:Reference number: S52929  
 A:Accession: S52929  
 A:Species: human immunodeficiency virus type 1, HIV-1  
 A:Molecule type: genomic RNA  
 A:Residues: 1-104 <STRT>  
 A:Cross-references: EMBL:X61357; NID:G60175; PIDN:CA43626.1; PID:G60176  
 C:Superfamily: type B retrovirus env polyprotein

Query Match 78.7%; Score 100; DB 2; Length 104;  
 Best Local Similarity 68.2%; Pred. No. 2, 2e-07;  
 Matches 15; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 LLSGCGKGRILCTTVQNMST 22  
 |||||:|||||:|||||:  
 Db 45 LNLWGCGKGRILCTTVQNMST 66

RESULT 4  
 521990 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Version: 100126 20  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C:Entry: 521990  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by HIV-1 RNA  
 A:Reference number: S21990  
 A:Accession: S21990  
 A:Species: human immunodeficiency virus type 1, HIV-1  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STRT>  
 A:Cross-references: EMBL:X61357; NID:G60175; PIDN:CA43626.1; PID:G60176  
 C:Superfamily: type B retrovirus env polyprotein

Query Match 65.4%; Score 83; DB 2; Length 357;  
 Best Local Similarity 59.1%; Pred. No. 0.00022;  
 Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 1 LLSGCGKGRILCTTVQNMST 22  
 |||||:|||||:|||||:  
 Db 93 LLSGCGKGRILCTTVQNMST 114

RESULT 5  
 522002 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Version: 100126 20  
 C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999  
 C:Accession: S54384  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by HIV-1 RNA  
 A:Reference number: S21990  
 A:Accession: S21990  
 A:Species: human immunodeficiency virus type 1, HIV-1  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STRT>  
 A:Cross-references: EMBL:X61357; NID:G60175; PIDN:CA43626.1; PID:G60176  
 C:Superfamily: type B retrovirus env polyprotein

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C:Entry: 522002  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by HIV-1 RNA  
 A:Reference number: S21990  
 A:Accession: S21990  
 A:Species: human immunodeficiency virus type 1, HIV-1  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STRT>  
 A:Cross-references: EMBL:X61357; NID:G60175; PIDN:CA43626.1; PID:G60176  
 C:Superfamily: type B retrovirus env polyprotein

Query Match 65.4%; Score 83; DB 2; Length 358;  
 Best Local Similarity 59.1%; Pred. No. 0.00018;  
 Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 1 LLSGCGKGRILCTTVQNMST 22  
 |||||:|||||:|||||:  
 Db 94 LLSGCGKGRILCTTVQNMST 115

RESULT 6  
 521990 env polyprotein p - human immunodeficiency virus type 1 (fragment)  
 N:Alternate names: coat protein gp41; carboxyl end of coat protein gp120  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Name: host homo sapiens (man)  
 C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
 C:Entry: 521990  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by HIV-1 RNA  
 A:Reference number: S21990  
 A:Accession: S21990  
 A:Species: human immunodeficiency virus type 1, HIV-1  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STRT>  
 A:Cross-references: EMBL:X61357; NID:G60175; PIDN:CA43626.1; PID:G60176  
 C:Superfamily: type B retrovirus env polyprotein

Query Match 65.4%; Score 83; DB 2; Length 443;  
 Best Local Similarity 59.1%; Pred. No. 0.00022;  
 Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 1 LLSGCGKGRILCTTVQNMST 22  
 |||||:|||||:|||||:  
 Db 332 LLSGCGKGRILCTTVQNMST 353

RESULT 7  
 522002 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Version: 100126 20  
 C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999  
 C:Accession: S54384  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by HIV-1 RNA  
 A:Reference number: S21990  
 A:Accession: S21990  
 A:Species: human immunodeficiency virus type 1, HIV-1  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STRT>  
 A:Cross-references: EMBL:X61357; NID:G60175; PIDN:CA43626.1; PID:G60176  
 C:Superfamily: type B retrovirus env polyprotein

submitted to the EMBL Data Library, July 1999

A:Accession: S54384  
A:Reference number: S54377  
A:Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-855 <THR>  
A:Cross-references: EMBL:M22639; NID:G329373; PIDN:AAA45370.1; PID:G329385  
C:Superfamily: type E retrovirus env polyprotein  
C:Superfamily: polyprotein

Query Match 65.4%; Score 83; DB 2; Length 855;

Best Local Similarity 59.1%; Pred. No. 0.00039; Mismatches 5; Indels 0; Gaps 0;

Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

DB 589 LLAGMGCKGRILCTTVPMNS 610

RESULT 8

env polyprotein precursor - simian immunodeficiency virus STVCP

A:Accession: S54384  
A:Reference number: S54377  
A:Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-855 <THR>  
A:Cross-references: EMBL:M22639; NID:G329373; PIDN:AAA45370.1; PID:G329385  
C:Superfamily: type E retrovirus env polyprotein  
C:Superfamily: polyprotein

Query Match 65.4%; Score 83; DB 2; Length 855;

Best Local Similarity 59.1%; Pred. No. 0.00039; Mismatches 5; Indels 0; Gaps 0;

Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

DB 589 LLAGMGCKGRILCTTVPMNS 610

RESULT 9

env polyprotein precursor - human immunodeficiency virus Zr-6

A:Accession: S54384  
A:Reference number: S54377  
A:Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-855 <THR>  
A:Cross-references: EMBL:M22639; NID:G329373; PIDN:AAA45370.1; PID:G329385  
C:Superfamily: type E retrovirus env polyprotein  
C:Superfamily: polyprotein

Query Match 65.4%; Score 83; DB 1; Length 855;

Best Local Similarity 54.5%; Pred. No. 0.00039; Mismatches 5; Indels 0; Gaps 0;

Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

DB 582 LLAGMGCKGRILCTTVPMNS 603

RESULT 9

env polyprotein precursor - human immunodeficiency virus Zr-6

A:Accession: S54384  
A:Reference number: S54377  
A:Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-855 <THR>  
A:Cross-references: EMBL:M22639; NID:G329373; PIDN:AAA45370.1; PID:G329385  
C:Superfamily: type E retrovirus env polyprotein  
C:Superfamily: polyprotein

Query Match 65.4%; Score 83; DB 1; Length 855;

Best Local Similarity 54.5%; Pred. No. 0.00039; Mismatches 5; Indels 0; Gaps 0;

Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

DB 582 LLAGMGCKGRILCTTVPMNS 603

C:Genetic: type E retrovirus env polyprotein

A:Accession: S54384

A:Reference number: S54377

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-855 <THR>

A:Cross-references: EMBL:M22639; NID:G329373; PIDN:AAA45370.1; PID:G329385

C:Superfamily: type E retrovirus env polyprotein

C:Superfamily: polyprotein

Query Match 65.4%; Score 83; DB 1; Length 855;

Best Local Similarity 59.1%; Pred. No. 0.00039; Mismatches 5; Indels 0; Gaps 0;

Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

DB 591 LLAGMGCKGRILCTTVPMNS 612

RESULT 10

env polyprotein gp120/gp41 - human immunodeficiency virus type 1

A:Accession: S52000

A:Reference number: S21990

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: EMBL:X61351; NID:G601044; PIDN:AAA45370.1; PID:G601085

C:Superfamily: type E retrovirus env polyprotein

C:Superfamily: polyprotein

Query Match 64.6%; Score 82; DB 2; Length 358;

Best Local Similarity 59.1%; Pred. No. 0.00025; Mismatches 6; Indels 0; Gaps 0;

Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

DB 94 LLAGMGCKGRILCTTVPMNS 115

RESULT 11

env polyprotein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment

A:Accession: S52000

A:Reference number: S21990

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: EMBL:X61351; NID:G601044; PIDN:AAA45370.1; PID:G601085

C:Superfamily: type E retrovirus env polyprotein

C:Superfamily: polyprotein

Query Match 64.6%; Score 82; DB 2; Length 358;

Best Local Similarity 59.1%; Pred. No. 0.00025; Mismatches 6; Indels 0; Gaps 0;

Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

DB 94 LLAGMGCKGRILCTTVPMNS 115

RESULT 12

env polyprotein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment

A:Accession: S52000

A:Reference number: S21990

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: EMBL:X61351; NID:G601044; PIDN:AAA45370.1; PID:G601085

C:Superfamily: type E retrovirus env polyprotein

C:Superfamily: polyprotein

Query Match 64.6%; Score 82; DB 2; Length 358;

Best Local Similarity 59.1%; Pred. No. 0.00025; Mismatches 6; Indels 0; Gaps 0;

Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

DB 94 LLAGMGCKGRILCTTVPMNS 115

```

822006
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 26-Aug-1999
C:Accession: S70420; S22006
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
Article: Distinct populations of human immunodeficiency virus type 1 in blood and cerebral
A:Reference number: S70417; NUID:92144209; PMID:1736940
A:Accession: S70420
A:Species: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STE2>
A:Cross-references: EMBL:X61354; NID:960190; PID:CAA43620.1; PID:960191
A:Experimental source: patient data library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
C:Superfamily: type E retrovirus env polypeptide
Query Match 63.0%; Score 80; DB 2; Length 357;
Best Local Similarity 54.5%; Pred. No. 0.00049;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 LLSGCKGRVLCYTSVQNNST 22
DB 93 LLSGCKGRVLCYTSVQNNST 114

RESULT 13
821994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 01-Dec-2000
C:Accession: S21994; S70421
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STE2>
A:Cross-references: EMBL:X61355; NID:960179; PID:CAA43622.1; PID:960180
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
Article: Distinct populations of human immunodeficiency virus type 1 in blood and cerebral
A:Reference number: S70417; NUID:92144209; PMID:1736940
A:Accession: S70421
A:Species: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STE2>
A:Cross-references: EMBL:X61355; NID:960179
C:Superfamily: type E retrovirus env polypeptide
Query Match 63.0%; Score 80; DB 2; Length 357;
Best Local Similarity 54.5%; Pred. No. 0.00049;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 LLSGCKGRVLCYTSVQNNST 22
DB 93 LLSGCKGRVLCYTSVQNNST 114

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```

A:Accession: S22004
A:Molecule type: DNA
A:Residues: 1-357 <STE2>
A:Cross-references: EMBL:X61353; NID:960188; PID:CAA43618.1; PID:960189
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
Article: Distinct populations of human immunodeficiency virus type 1 in blood and cerebral
A:Reference number: S70417; NUID:92144209; PMID:1736940
A:Accession: S70420
A:Species: preliminary
A:Molecule type: DNA
A:Residues: 1-294-357 <STE2>
A:Cross-references: EMBL:X61353; NID:960188
C:Superfamily: type E retrovirus env polypeptide
Query Match 63.0%; Score 80; DB 2; Length 357;
Best Local Similarity 54.5%; Pred. No. 0.00049;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 LLSGCKGRVLCYTSVQNNST 22
DB 93 LLSGCKGRVLCYTSVQNNST 114

RESULT 15
821996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 26-Aug-1999
C:Accession: S70422; S21996
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
Article: Distinct populations of human immunodeficiency virus type 1 in blood and cerebral
A:Reference number: S70417; NUID:92144209; PMID:1736940
A:Accession: S70422
A:Species: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STE2>
A:Cross-references: EMBL:X61356; NID:960181; PID:CAA43624.1; PID:91067129
A:Experimental source: patient 27L
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polypeptide
Query Match 63.0%; Score 80; DB 2; Length 357;
Best Local Similarity 54.5%; Pred. No. 0.00049;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 LLSGCKGRVLCYTSVQNNST 22
DB 93 LLSGCKGRVLCYTSVQNNST 114

```

Search completed: May 29, 2003, 10:40:24  
Job time : 10.8254 sec

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: May 29, 2003, 10:31:50 | Search time 5.4127 Seconds  
(without alignments)

168,581 Million cell updates/sec

Title: US-09-147-362A-5

Sequence: 127

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

1 number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_40.\*

Result No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

Result No. Score Match Length DB ID Description

1 83 65.4 853 1 ENV\_HV122 P12487 human immun

2 83 65.4 853 1 ENV\_HV122 P12487 human immun

3 83 65.4 853 1 ENV\_HV122 P12487 human immun

4 80 63.0 843 1 ENV\_HV122 P12487 human immun

5 80 63.0 843 1 ENV\_HV122 P12487 human immun

6 80 63.0 843 1 ENV\_HV122 P12487 human immun

7 80 63.0 843 1 ENV\_HV122 P12487 human immun

8 80 63.0 843 1 ENV\_HV122 P12487 human immun

9 80 63.0 843 1 ENV\_HV122 P12487 human immun

10 80 63.0 843 1 ENV\_HV122 P12487 human immun

11 80 63.0 843 1 ENV\_HV122 P12487 human immun

12 80 63.0 843 1 ENV\_HV122 P12487 human immun

13 80 63.0 843 1 ENV\_HV122 P12487 human immun

14 80 63.0 843 1 ENV\_HV122 P12487 human immun

15 80 63.0 843 1 ENV\_HV122 P12487 human immun

16 80 63.0 843 1 ENV\_HV122 P12487 human immun

17 80 63.0 843 1 ENV\_HV122 P12487 human immun

18 80 63.0 843 1 ENV\_HV122 P12487 human immun

ALIGNMENTS

Sequence: 127

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

1 number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_40.\*

Result No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

Result No. Score Match Length DB ID Description

1 83 65.4 853 1 ENV\_HV122 P12487 human immun

2 83 65.4 853 1 ENV\_HV122 P12487 human immun

3 83 65.4 853 1 ENV\_HV122 P12487 human immun

4 80 63.0 843 1 ENV\_HV122 P12487 human immun

5 80 63.0 843 1 ENV\_HV122 P12487 human immun

6 80 63.0 843 1 ENV\_HV122 P12487 human immun

7 80 63.0 843 1 ENV\_HV122 P12487 human immun

8 80 63.0 843 1 ENV\_HV122 P12487 human immun

9 80 63.0 843 1 ENV\_HV122 P12487 human immun

10 80 63.0 843 1 ENV\_HV122 P12487 human immun

11 80 63.0 843 1 ENV\_HV122 P12487 human immun

12 80 63.0 843 1 ENV\_HV122 P12487 human immun

13 80 63.0 843 1 ENV\_HV122 P12487 human immun

14 80 63.0 843 1 ENV\_HV122 P12487 human immun

15 80 63.0 843 1 ENV\_HV122 P12487 human immun

16 80 63.0 843 1 ENV\_HV122 P12487 human immun

17 80 63.0 843 1 ENV\_HV122 P12487 human immun

P05683 human immun

P12487 human immun

P12487 human immun

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FT	CHAIN	501	854	TRANSMEMBRANE	GLYCOPROTEIN.	POTENTIAL.
FT	501	854	517			

CC  
--  
EMBL: K03458; AAA5380.1; --  
PIR: D26192; VCLJZR.  
DR



[illegible][illegible]



[illegible]

Query	Local Similarity	Score	DB1	Length	DB2
Bacter	54.5%	1.0	1.0	1.0	1.0
FT CARBOHYD	2.6	2.6	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	2.6	2.6	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	2.6	2.6	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	3.32	3.32	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	3.39	3.39	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	3.56	3.56	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	3.86	3.86	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	3.92	3.92	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	4.01	4.01	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	4.43	4.43	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	4.58	4.58	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	6.06	6.06	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	6.20	6.20	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	6.32	6.32	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	6.69	6.69	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	7.45	7.45	N-LINKED (GLCNAc. .)	(POTENTIAL)	
FT CARBOHYD	8.11	8.11	N-LINKED (GLCNAc. .)	(POTENTIAL)	
50 SEQUENCES	851 AA;	96644 MW;	D16A3C90857785F1 CKEG4		

Accession	Sequence	Length	Score	E-value	Ident	Start	End	Frame	Strand	Model	Gene	Product	Organism	Accession	Length	Score	E-value	Ident	Start	End	Frame	Strand	Model	Gene	Product	Organism	
QY	1 LL0SGCKEALVCTYSVQAKST	22	100	0.00	100	1	22	0	+	1	LL0SGCKEALVCTYSVQAKST	22	0.00	100	100	100	0.00	100	1	22	0	+	1	LL0SGCKEALVCTYSVQAKST	22	0.00	100
Dh	587 LELGMSGGLICTIVAPNMS	608	100	0.00	100	1	608	0	+	1	LELGMSGGLICTIVAPNMS	608	0.00	100	100	100	0.00	100	1	608	0	+	1	LELGMSGGLICTIVAPNMS	608	0.00	100



CC	FT	DISLAF1	383	416	BY SIMILARITY.
CC	FT	CAROHYD	88	88	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	136	136	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	141	141	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	156	156	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	166	166	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	186	186	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	195	195	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	233	232	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	239	239	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	260	260	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	274	274	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	287	287	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	297	297	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	299	299	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	330	330	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	354	354	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	384	384	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	390	390	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	395	395	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	400	400	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	461	461	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	609	609	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	614	614	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	623	623	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	635	635	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	672	672	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	748	748	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	FT	CAROHYD	818	818	N-LINKED (GLCNAC. ) (POTENTIAL).
CC	SEQ	SEQUENCE	853 AA;	9612 MW;	337B9385672AAB_CG64; (POTENTIAL).
CC	Query Match		6.0%;	Score 80;	DB 1;
CC	Best Local Similarity		54.5%;	Score No. 0.0011;	Length 853;
CC	Matches	12;	Conservative	5;	Mismatches 5;
CC					Indels 0;
CC					Gaps 0.
CC	Qy	1	ILDSKCKEGLTCTVYCNMST	22	
CC	Db	590	ILGIMSGKGLTCTVYCNMHS	611	
CC	ENV_HVLA1				
CC	RESULT 11				
CC	ID	ENV_HVLA2	STANDARD;	PRF.	855 AA.
CC	AC	P03378.1	(Ref.)	01.	(Created)
CC	DT	21-JUL-1986	(Ref.)	01.	(Last annotation update)
CC	DT	15-JUL-1999	(Ref.)	38.	(Last annotation update)
CC	DE	Envelope polypeptide gp160 precursor (Contains: Exterior membrane glycoprotein (gp120), Transmembrane glycoprotein (gp41)).			
CC	GN	ENV.			
CC	OS	Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).			
CC	VS	Viruses; Retrod viruses; Retroviridae; Lentivirus.			
CC	PA	ENV_TaxId:1685;			
CC	RA	SEQUENCE FROM N.A.			
CC	RP	MEDLINE:85090453; PubMed:2578272;			
CC	RA	Sanchez-Pescador R., Power M.D., Barr P.J., Stelmer K.S.,			
CC	RA	Stempkin M.M., Brown-Shiner S.L., Gee W.W., Renard A., Randolph A.,			
CC	RA	Levy D.A., Dina D., Luciw P.A.;			
CC	FT	Nucleotide sequence and expression of an AIDS-associated retrovirus			
CC	RL	Science 227:484-497(1985).			
CC	CC	This EMBL-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as the content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@ebi.ac.uk.			
CC	EMBL;	K02007; AA059882.1; -			





OS	Human immunodeficiency virus type-1 (HIV-1).
CC	Viruses; Retroviridae; Lentivirus.
NCBI	TaxId=82834.
OX	(1)
RN	SEQUENCE FROM N.A.
RA	RefSeq:U095127.1; PubMed:762669.
RP	Hellwig E, Kottmann C, von der Hofe M., Lautenberger J, Hahn B.M., Shaw G.W., Koenig L.I., Weiss R.B., Weisberg D., Gallo R.C., Blattner W.R.
RT	viral variability, and serum antibody response in a laboratory worker infected with HIV type 1 (HTLV type IIIS). "
FT	AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
CC	-----
CC	This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Molecular Biology Laboratory, Heidelberg. The sequence may be used by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-eb.ch/announce/">http://www.isb-eb.ch/announce/</a> or send an email to <a href="mailto:license@isb-eb.ch">license@isb-eb.ch</a> ).
CC	-----
DR	EMBL, U12055; AAA76690.1. ;
DR	GlycoScoutDB, U095127.1; RefSeq:U095127.1; GenBank, U095127.1;
DR	InterPro, IPR000777; GP120_1.
DR	Pfam, PF00516; GP120_1.
KW	AIDS; Coat protein; Glycoprotein; Glycoprotein; Transmembrane; signal.
FT	SIGNAL 1 30
FT	CDS 31 51
FT	CHAIN 52 81
FT	DISULFID 54 74
FT	DISULFID 119 205
FT	DISULFID 126 196
FT	DISULFID 131 157
FT	DISULFID 218 247
FT	DISULFID 228 239
FT	DISULFID 328 378
FT	DISULFID 385 418
FT	CARBOHYD 88 88
FT	CARBOHYD 136 136
FT	CARBOHYD 141 141
FT	CARBOHYD 150 150
FT	CARBOHYD 156 160
FT	CARBOHYD 160 166
FT	CARBOHYD 169 195
FT	CARBOHYD 230 230
FT	CARBOHYD 241 244
FT	CARBOHYD 241 241
FT	CARBOHYD 262 262
FT	CARBOHYD 276 276
FT	CARBOHYD 289 289
FT	CARBOHYD 290 295
FT	CARBOHYD 301 303
FT	CARBOHYD 332 332
FT	CARBOHYD 339 339
FT	CARBOHYD 356 356
FT	CARBOHYD 366 386
FT	CARBOHYD 392 392
FT	CARBOHYD 397 397
FT	CARBOHYD 400 400
FT	CARBOHYD 448 448
FT	CARBOHYD 463 463
FT	CARBOHYD 611 611
FT	CARBOHYD 616 616
FT	CARBOHYD 624 624
FT	CARBOHYD 637 637
FT	CARBOHYD 674 674
FT	CARBOHYD 674 674
FT	CARBOHYD 816 816
SE	SEQUENCE 856 AA; 9639 MW; DC2413JCCT7B6687 CMCK4;

Thu May 29 15:25:44 2003

us-09-147-362a-5.rsp

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Query Match Similarity      69.0%; Score 80; DB 1; Length 856;
Best Local Similarity     54.5%; Pred. No. 0.0001;
Matches       12; Conservative    5; Mismatches   5; Indels   0; Gaps   0.

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QY          1 HDSGGCGGAGTCTCAGTCSTONEST 22
              ||| | |||||
Db         592 LHSIGWCSGRGLCTTTAAVPMNAS 613

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Search completed: May 29, 2003, 10:36:59
Job time : 6.4127 secs

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AC  G9D0L3;
DT  01-MAR-2001 (TRENBLREL. 16, Created)
DT  01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT  01-DEC-2001 (TRENBLREL. 15, Last annotation update)
DR  Envelope glycoprotein (Fragment).
ENV  Envelope glycoprotein (Fragment).
OC  Human immunodeficiency virus type 1.
OC  Viruses; Retroid viruses; Retroviridae; Lentivirus.
OK  NCBI_TaxID=11676;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=SP-M1321;
RC  MEDLINE=2054646; PubMed=1153079;
RA  Philippe M.; Robertson D.; Soudine S.; Zorrano A.;
RA  Vialto J.; Salas A.; Lopez R.; Rodriguez A.;
RT  Molecular Characterization of Non-B HIV Type 1 Subtypes from Africa
RL  In Spain.
RL  AIDS Res. Hum. Retroviruses 16:1967-1971(2000).
EMBL: AF255339; AAC6894.1;
Fasta: AF255339; AAC6894.1;
InterPro: IPR000328; Env_GP41.
KW  Transmembrane; GP41; 1.
FT  NON_TER 1 1
FT  NON_TER 135 135
SQ  SEQUENCE 135 AA; 16285 MW; D34B9E7731BB836 CRC64;

Query Match
Best Local Similarity 89.8%; Score 114; DB 15; Length 135;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 L10SGCKGRALVCTSYVNMST 22
Db 48 L10SGCKGRALVCTSYVNMST 69

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RESULT 3
O9IEC3 PRELIMINARY; PRT; 216 AA.
AC  G9IEC3;
DT  01-OCT-2000 (TRENBLREL. 15, Created)
DT  01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT  01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE  GP41 (Fragment).
ENV  GP41 (Fragment).
GN  ENV.
OS  Human immunodeficiency virus type 1.
OC  Viruses; Retroid viruses; Retroviridae; Lentivirus.
OK  NCBI_TaxID=11676;
RP  SOURCE FROM N.A.
RC  STRAIN=RC07;
RA  Roques P.; Robertson D.; Sandrine S.; Christel D.; Francois S.;
RA  Philippe M.;
RT  Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.
RT  Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AJ236399; CAB86243.1;
Fasta: AJ236399; CAB86243.1;
InterPro: IPR00517; GP41; 1.
KW  Transmembrane; GP41; 1.
FT  NON_TER 1 1
FT  NON_TER 216 216
SQ  SEQUENCE 216 AA; 25027 MW; 413AB9B8F1BFC9A CRC64;

Query Match
Best Local Similarity 89.8%; Score 114; DB 15; Length 216;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 L10SGCKGRALVCTSYVNMST 22
Db 47 L10SGCKGRALVCTSYVNMST 68

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ID  G9IEC3 PRELIMINARY; PRT; 242 AA.
AC  G9IEC3;
DT  01-MAR-2001 (TRENBLREL. 15, Created)
DT  01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT  01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DR  TM, GP41 (Fragment).
ENV  TM, GP41 (Fragment).
GN  TM.
OS  Human immunodeficiency virus type 1.
OC  Viruses; Retroid viruses; Retroviridae; Lentivirus.
OK  NCBI_TaxID=11676;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BCP112;
RA  Roques P.; Robertson D.; Souquiere S.; Diamond F.; Mauchere P.;
RA  Depienne C.; Brun-Vezinet F.; Dormont D.; Simon F.;
RT  Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates.
RT  Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AJ241366; CAB86336.1;
Fasta: AJ241366; CAB86336.1;
InterPro: IPR000328; Env_GP41.
KW  Pfam; PFO0517; GP41; 1.
DR  Pfam; PFO0517; GP41; 1.
KW  Transmembrane; GP41; 1.
FT  NON_TER 1 1
FT  NON_TER 242 242
SQ  SEQUENCE 242 AA; 27539 MW; DE8A73D0F08A6FD7 CRC64;

Query Match
Best Local Similarity 89.8%; Score 114; DB 15; Length 242;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 L10SGCKGRALVCTSYVNMST 22
Db 64 L10SGCKGRALVCTSYVNMST 85

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RESULT 5
O9IEC3 PRELIMINARY; PRT; 214 AA.
AC  G9IEC3;
DT  01-MAR-2001 (TRENBLREL. 15, Created)
DT  01-MAR-2001 (TRENBLREL. 15, Last sequence update)
DT  01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE  GP41 protein (Fragment).
ENV  GP41 protein (Fragment).
GN  ENV.
OS  Human immunodeficiency virus type 1.
OC  Viruses; Retroid viruses; Retroviridae; Lentivirus.
OK  NCBI_TaxID=11676;
RP  SOURCE FROM N.A.
RC  STRAIN=BCP120;
RA  Roques P.; Robertson D.; Diamond F.; Souquiere S.; Mauchere P.;
RA  Depienne C.; Brun-Vezinet F.; Dormont D.; Simon F.;
RT  Phylogenetic analysis of 48 newly derived HIV-1 group O strains: High
RT  viral diversity.
RT  Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AJ298125; CAB8806.1;
Fasta: AJ298125; CAB8806.1;
InterPro: IPR000328; Env_GP41.
DR  InterPro; IPR000328; Env_GP41.
KW  Transmembrane; GP41; 1.
FT  NON_TER 1 1
FT  NON_TER 214 214
SQ  SEQUENCE 214 AA; 24436 MW; FFA890D08F6A1AB CRC64;

Query Match
Best Local Similarity 88.2%; Score 112; DB 15; Length 214;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 L10SGCKGRALVCTSYVNMST 22
Db 45 L10SGCKGRALVCTSYVNMST 66

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RESULT 4  
O9IEC3

RESULT 6  
O11941

ID	Accession	Source	Strain	Length	Score	Pos	Indels	Gaps
01	011941	PRELIMINARY	PRT, 116 AA.					
AC	011941							
DT	01-JUL-1997	(TEMBELZEL_04, Created)						
DT	01-JUL-1997	(TEMBELZEL_04, Last sequence update)						
DT	01-DEC-2001	(TEMBELZEL_19, Last annotation update)						
CR	EMV	Envelope glycoprotein (fragment).						
CS	Human immunodeficiency virus type 1							
OX	Viruses; Retrovid viruses; Retroviridae; Lentivirus.							
NCBI	_Taxid=11676,							
LN	[1]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=ABT124;							
RC	EMDID=97340911; PubMed:9197385;							
RA	Brennan C.A., Hackett D.J., Zekun L., Lund J.K., Vallert A.S.,							
RA	Hickman R.K., Gutler L., Kapelle U., von Overbeck U., Hampf H.,							
RA	Recht S.G., glyptery immunodominant region of HIV type 1 group O from							
RT	West central Africa,"							
	AIDS Res. Hum. Retroviruses 13:901-904(1997).							
	EMBL: U90134; AAB62817.1; -							
	InterPro: IP8000328; EHV_Gp41.							
	Pfam: PF00517; Gp41; 1.							
DR								
FT	NON_TER							
FT	NON_TER							
KW	transmembrane.							
QY	SEQUENCE							
QY	116 AA; 13789 MW; 488A9A40F4255E3E CRC64;							
Match	87.4%; Score 111; DB 15; Length 116;							
Match	Best Local Similarity: 81.8%; Pstd. No. 5.1e-10;							
Match	Matches 18; Conservative 2; Mismatches 0; Gaps 0;							

	RESULT 7	
O040458	PRELIMINARY:	PRT; 116 AA.
ID O040458		
CD O040458	(T-EMBL)rel. 05_Created)	
DT 01-JAN-1998	(T-EMBL)rel. 05, last sequence update)	
DT 01-JAN-1998	(T-EMBL)rel. 05, last annotation update)	
OS DEC-2001	(T-EMBL)rel. 05, last annotation update)	
DE Envelope transmembrane glycoprotein (Fragment).		
DS Human immunodeficiency virus type 1.		
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.		
OX NCBI_TaxID=11676;		
RY 111		
RS SEQUENCE FROM N.A.		
RZ STRAIN=GROUP O		
RA RBibollat-Ruche F., Ekasa E., Peeters M., Delaporte E.;		
RA "Molecular characterization of envelope transmembrane glycoprotein of		
RT 14 new human immunodeficiency virus type 1 group O strains from		
RT different African countries."		
RL Submitted (DEC-1996) to the EMBL/Danbank/DBJ databases.		
RD EMBL: Y097744; CAI:Y097744; ...		
RD GenBank: AF050046; DDBJ: AF050046.		
RD Trimeric PR0517 CD41, 1.		
RD Transmembrane.		
KW TRANSMEMBRANE.		
KW NON TER	1	
FT NON TER	116	116
SO SEQUENCE	116 AA; 13865 MW; 540FSD3B7AD8A9D8 CRC64;	
Query Match	87.4%; Score 111; DB 15; Length 116;	
Ident Locally	Similarity: 11.8%; 1; Identical: NO 12-10;	
Matches	Conservative: 1; Miscellaneous: 0; Gaps: 0	
Cy	L LQSMGCKRRLCTVSYVNANKT 22	
Dd	1 LQSMGCKRRLCTVSYVNANKT 60	

	RESULT 8	
Q9IH09	PREMITINARI;	PRT, 130 AA.
ID Q9IH09		
DT 01-OCT-2000	(TRMBHLref), 15, Created	
DT 01-OCT-2000	(TRMBHLref), 15, Last sequence update)	
DE 01-DEC-2001	(TRMBHLref), 19, Last annotation update)	
DE Envelope glycoprotein (Fragment).		
GN GP41.		
OS Human immunodeficiency virus type 1,		
OC Viruses; Retrofod viruses; Retroviridae; Lentivirus.		
CC NCBI_TaxId=1676;		
RN		
RP SEQUENCE FROM N.A.		
RC STRAIN=97CM798;		
RA MEDLINE=40386754; PubMed=10933623;		
RA Yang C., Gao F., Fontignat R.N., Zekeng L., van der Groen G.,		
RA Plehnke D., Schablik C., Lal R.B.,		
RT "Phylogenetic analysis of processes and transmembrane regions of HIV		
RT type 1 group O."		
RL AIDS Res Hum. References 16:1075-1081(2000).		
DL Interpro: IPR001912; EMBL:U012.		
DR InterPro: IPR001912; ECV_GP41.		
DR Pfam: PF00517; GP41, 1.		
KW Transmembrane.		
FT NON TER	1	1
FT NON_TER	130	130
SQ SEQUENCE	130 AA; 15S93 MW; 5385789A36344EA CRC64;	
Query Match		
% Identity	87.4%; Score 111; DB 15;	
% Similarity	81.0%; Pctd No. 5; 8e-10;	
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;		
QY	1 LLSSGCKSGALVCTYSVMNST 22	
DB		
db	40 LLNSGCKSGALVCTYSVKMNT 61	

[illegible]

## RESULT 10

Q91E95 PRELIMINARY; PRT: 218 AA.

AC Q91E95; 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

GN GP41 (Fragment).

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI\_TaxId=11676;

RN NCBI\_Locus=U011676.1

RP STRAIN=BF551;

RA Philippe M.;

RT Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.

RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.

DR InterPro: IPR000328; EMBL\_GP41.

DR Pfam: PF00517; GP41; 1.

KW Transmembrane

FT NON\_TER 1 218

SQ SEQUENCE 218 AA; 25243 MW; 87F0E1E20E79FA8 CRC64;

Query Match 87.4%; Score 111; DB 15; Length 218;

Best Local Similarity 77.3%; Pctd No. 9 7e-12;

Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLOSCKGRJVCYSVQNNST 22

Db 54 LLSMGCKRGLICTYSVKNST 75

## RESULT 11

Q91E95

AC Q91E95; 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

GN GP41 (Fragment).

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI\_TaxId=11676;

RN NCBI\_Locus=U011676.1

RP STRAIN=BF551;

RA Philippe M.;

RT Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.

RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.

DR InterPro: IPR000328; EMBL\_GP41.

DR Pfam: PF00517; GP41; 1.

KW Transmembrane

FT NON\_TER 1 220

SQ SEQUENCE 220 AA; 25503 MW; BD67E4C8BD40BD1 CRC64;

Query Match 87.4%; Score 111; DB 15; Length 220;

Best Local Similarity 81.8%; Pctd No. 9 8e-10;

Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LLOSCKGRJVCYSVQNNST 22

Db 53 LLSMGCKRGLICTYSVKNST 74

## RESULT 12

Q91ED2 PRELIMINARY; PRT: 512 AA.

AC Q91ED2; 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

GN Env Polyprotein (Fragment).

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI\_TaxId=11676;

RN NCBI\_Locus=U011676.1

RP STRAIN=BF551;

RA Philippe M.;

RT Phylogenetic analysis of C2-GP41 region.

RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.

DR InterPro: IPR000328; EMBL\_GP41.

DR Pfam: PF00517; GP120; 1.

KW Transmembrane

FT NON\_TER 1 512

SQ SEQUENCE 512 AA; 57977 MW; 4F658B2C15CE492 CRC64;

Query Match 87.4%; Score 111; DB 15; Length 512;

Best Local Similarity 81.8%; Pctd No. 2 3e-09;

Matches 18; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LLOSCKGRJVCYSVQNNST 22

Db 372 LLSMGCKRGLICTYSVKNST 393

## RESULT 13

Q91ED5

AC Q91ED5; 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

GN Env Polyprotein (Fragment).

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI\_TaxId=11676;

RN NCBI\_Locus=U011676.1

RP STRAIN=BF551;

RA Philippe M.;

RT Phylogenetic analysis of C2-GP41 region.

RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.

DR InterPro: IPR000328; EMBL\_GP41.

DR Pfam: PF00517; GP120; 1.

KW Transmembrane

FT NON\_TER 1 538

SQ SEQUENCE 538 AA; 60777 MW; B3C9E6A233FEED1 CRC64;

Query Match 87.4%; Score 111; DB 15; Length 538;

Best Local Similarity 77.3%; Pctd No. 2 4e-09;

Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLOSCKGRJVCYSVQNNST 22

Db 1 LLSMGCKRGLICTYSVKNST 74



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1	137	100.0	22	19	AAAB0466	Peptide derived E
2	124	97.6	22	19	AAAB0466	Peptide derived E
3	124	97.6	22	19	AAAB0466	Peptide derived E
4	111	96.3	22	19	AAAB0466	Peptide derived E
5	111	96.3	22	19	AAAB0466	Peptide derived E
6	119	95.7	22	19	AAAB0466	Peptide derived E
7	117	95.1	40	17	AAAB0466	Peptide derived E
8	117	95.1	40	17	AAAB0466	Peptide derived E
9	116	94.3	22	19	AAAB0466	Peptide derived E
10	116	94.3	22	19	AAAB0466	Peptide derived E
11	115	93.6	22	19	AAAB0466	Peptide derived E
12	115	93.6	22	19	AAAB0466	Peptide derived E
13	114	89.8	32	19	AAAB0470	Peptide derived E

11	113	89.0	22	19	AAW80459
12	113	89.0	32	12	AAW80471
13	110	86.6	40	17	AAW07352
14	110	86.6	113	20	AAW05565
15	110	86.6	205	21	AAW77333
16	110	86.6	210	21	AAW77333
17	110	86.6	215	20	AAW77332
18	110	86.6	215	20	AAW77332
19	110	86.6	245	20	AAW04933
20	110	86.6	245	20	AAW06977
21	110	86.6	245	21	AAW77336
22	110	86.6	281	20	AAW05457
23	110	86.6	373	20	AAW08305
24	110	86.6	373	20	AAW06979
25	110	86.6	460	20	AAV05940
26	110	86.6	460	20	AAV05940
27	110	86.6	472	21	AAW77321
28	110	86.6	472	21	AAW77321
29	110	86.6	488	20	AAV05654
30	110	86.6	490	20	AAV04944
31	110	86.6	490	20	AAW06978
32	110	86.6	490	21	AAW77330
33	110	86.6	526	20	AAW05455
34	110	86.6	618	20	AAV04960
35	110	86.6	618	21	AAW77332
36	110	86.6	618	21	AAW77332
37	110	86.6	706	20	AAV05625
38	110	86.6	706	20	AAV05625
39	110	86.6	732	20	AAW05502
40	110	86.6	873	20	AAW05951
41	110	86.6	873	20	AAV06955
42	110	86.6	873	21	AAW77336
43	109	85.8	104	17	AAW07245
44	108	85.3	33	21	AAW12232
45	107	84.3	33	21	AAW12231

RESULT 1  
AAW80466  
ID AAW80466 standard; peptide; 22 AA

DT 28-JAN-1999 (first entry)  
XX  
DE Peptide derived from a conserved sequence of group O human HIV.

KW Group O human immune deficiency virus; HIV; detection; infection

OS Immune deficiency virus.

PN W09845323-A1

PD 15-OCT-1998

PF 06-APR-1998; 98WO-FR00691.  
YY

PR 24-FEB-1998; 98FR-0002212.  
PR 09-APR-1997; 97FR-0004356.

XX  
PA (SNFI ) PASTEUR SANOFI DIAGN

AA Chenebaux DMB, Delagneau JFH, Gadel  
PI

DR WPI; 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by

XX

PS Claim 6; Page 43; 55pp; French.

XX AA80459-74 represent synthetic peptides (either linear or cyclized by  
CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
CC connected around short highly conserved sequences present in isolates  
CC of group O human immune deficiency virus (HIV). The peptides are  
CC useful as immunological reagents for detecting infection by group O  
CC human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 100.0%; Score 127; DB 19; Length 22;  
Best Local Similarity 100.0%; Pred. No. 96-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLSNGCRGLVCTYSQVNMET 22  
Db 1 LLSNGCRGLVCTYSQVNMET 22

RESULT 2

AA80461 standard; peptide; 22 AA.

XX 28-JAN-1999 (first entry)  
XX Peptide derived from a conserved sequence of group O human HIV.  
XX Group O human immune deficiency virus; HIV; detection; infection.

XX Synthetic.  
XX Immune deficiency virus.

XX MO9845323-A1.

XX 15-OCT-1998.

XX 06-APR-1998; 98MO-FR00691.

XX 24-FEB-1998; 98FR-0002212.

XX 09-APR-1997; 97FR-0004356.

XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.

XX Cheneboux DMB, Delagrange JFH, Gabelle SJX, Rieunier FY;

XX WPI: 1998-581390/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
PT human immune deficiency virus of group O

XX Claim 6; Page 42; 55pp; French.

XX AA80459-74 represent synthetic peptides (either linear or cyclized by  
CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
CC connected around short highly conserved sequences present in isolates  
CC of group O human immune deficiency virus (HIV). The peptides are  
CC useful as immunological reagents for detecting infection by group O  
CC human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 97.6%; Score 124; DB 19; Length 22;  
Best Local Similarity 95.5%; Pred. No. 2,26-09;  
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLSNGCRGLVCTYSQVNMET 22  
Db 1 LLSNGCRGLVCTYSQVNMET 22

RESULT 3

AA80460 standard; peptide; 22 AA.

XX 28-JAN-1999 (first entry)

XX Peptide derived from a conserved sequence of group O human HIV.  
XX Group O human immune deficiency virus; HIV; detection; infection.

XX Synthetic.  
XX Immune deficiency virus.

XX MO9845323-A1.

XX 15-OCT-1998.

XX 06-APR-1998; 98MO-FR00691.

XX 24-FEB-1998; 98FR-0002212.

XX 09-APR-1997; 97FR-0004356.

XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.

XX Cheneboux DMB, Delagrange JFH, Gabelle SJX, Rieunier FY;

XX WPI: 1998-581390/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
PT human immune deficiency virus of group O

XX Claim 6; Page 42; 55pp; French.

XX AA80459-74 represent synthetic peptides (either linear or cyclized by  
CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
CC connected around short highly conserved sequences present in isolates  
CC of group O human immune deficiency virus (HIV). The peptides are  
CC useful as immunological reagents for detecting infection by group O  
CC human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 95.3%; Score 121; DB 19; Length 22;  
Best Local Similarity 95.5%; Pred. No. 1,36-09;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLSNGCRGLVCTYSQVNMET 22  
Db 1 LLSNGCRGLVCTYSQVNMET 22

RESULT 4

AA80469 standard; peptide; 32 AA.

XX 28-JAN-1999 (first entry)

XX Peptide derived from a conserved sequence of group O human HIV.  
XX Group O human immune deficiency virus; HIV; detection; infection.

XX Synthetic.  
XX Immune deficiency virus.

XX MO9845323-A1.

XX 15-OCT-1998.

XX 06-APR-1998; 98MO-FR00691.



XX 24-FEB-1998; 98FR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 PA (SNP1) PASTEUR SANOPI DIAGNOSTICS SA.  
 PI Chenchaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;  
 DR WPI: 1998-581390/49.  
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by  
 XX human immune deficiency virus of group O  
 PS Claim 6; Page 44; 55pp; French.  
 CC AA080459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 XX human immune deficiency virus (HIV).  
 SO Sequence 32 AA;  
 Query Match 94.5%; Score 120; DB 19; Length 32;  
 Best Local Similarity 90.9%; Pred. No. 1e-08; 0; Indels 0; Gaps 0;  
 Matches 20; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LLSWCGCGRLVCYTSYONNET 22  
 DB 11 LLSWCGCGRLVCYTSYONNET 32  
 RESULT 5  
 ID AA080462  
 AC AA080462 standard; peptide; 22 AA.  
 XX AA080462;  
 XX 28-JUN-1999 (first entry)  
 DT XX  
 XX Peptide derived from a conserved sequence of group O human HIV.  
 XX Group O human immune deficiency virus; HIV; detection; infection.  
 OS Synthetic.  
 OS Immune deficiency virus.  
 MO9845323-A1.  
 PD 15-OCT-1998.  
 XX 06-APR-1998; 98MO-FR00691.  
 XX 24-FEB-1998; 98FR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 PA (SNP1) PASTEUR SANOPI DIAGNOSTICS SA.  
 PI Chenchaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;  
 DR WPI: 1998-581390/49.  
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by  
 XX human immune deficiency virus of group O  
 PS Claim 6; Page 42; 55pp; French.  
 CC AA080459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O

CC human immune deficiency virus (HIV).  
 XX Sequence 22 AA;  
 SO 93.7%; Score 119; DB 19; Length 22;  
 Query Match 90.9%; Pred. No. 9.6e-09;  
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 LLSWCGCGRLVCYTSYONNET 22  
 DB 1 LLSWCGCGRLVCYTSYONNET 22  
 RESULT 6  
 ID AA007346  
 AC AA007346 standard; peptide; 40 AA.  
 XX AA007346;  
 XX 03-JUN-1997 (first entry)  
 DT XX  
 XX Partial sequence of gp41 from HIV-1 gp. O strain BCF07 (MAN).  
 DE Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;  
 FM C23-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;  
 KM Primer; hybridisation; amplification; PCR; polymerase chain reaction;  
 XX Immunogen; antibody.  
 OS Human immunodeficiency virus type 1.  
 XX W09627013-A1.  
 PD 06-SEP-1996.  
 XX 26-FEB-1996; 96MO-FR00294.  
 PR 27-FEB-1995; 95FR-0002236.  
 XX (ASST.) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
 PA (INRA) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX Châix-Baudier M., Loussert-Ajaka I., Ly T., Sargostel S., Simon F.  
 DR WPI: 1996-412779/41.  
 DR N-PSDB; AAT43922.  
 XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
 PF antibodies - useful for diagnosis, screening and typing, or as  
 PF immunogens  
 PS Claim 12; Page 34; 71pp; French.  
 CC Human immunodeficiency virus type 1 (HIV-1) strains are currently  
 CC divided into 2 major groups based on the nucleotide sequences of the  
 CC envelope gene (env): group M containing sub-groups A-G, and group O  
 CC containing the strains ANR70 and WY9180. The invention relates to the  
 CC discovery of several sequences of the C23-env gp41 and gag genes (see  
 CC AAT44907-39 and AAT07323-64). The novel strains have been deposited as  
 CC retrovirusesc NCIM I-1544 (BCF02 (EBS)), 1543 (BCF01 (PAN)), 1546 (BCF07  
 CC (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence  
 CC presented here is from the strain BCF07 (MAN) and corresponds to a  
 CC fragment of the gp41 protein encoded by the env gene. The nucleic acids  
 CC can be used to detect gp. O HIV-1 strains by hybridization or as  
 CC primers for amplification of the gp41 gene by polymerase chain reaction.  
 CC The peptides encoded by the nucleic acids can be used as immunogens  
 CC to raise Ab for detecting gp. O HIV-1.  
 SO Sequence 40 AA;  
 Query Match 92.1%; Score 117; DB 17; Length 40;  
 Best Local Similarity 80.4%; Pred. No. 3e-08; 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWGCGRGLVCTSYVQNNET 22  
 DB 19 LLSWGCGRGLVCTSYVQNNET 40

RESULT 7  
 AA080464 standard; peptide: 22 AA.  
 AA080464:  
 AA080464:  
 28-JAN-1999 (first entry)  
 Peptide derived from a conserved sequence of group O human HIV.  
 DE Peptide derived from a conserved sequence of group O human HIV.  
 XX Group O human immune deficiency virus; HIV; detection; infection.  
 KM Synthetic.  
 OS Immune deficiency virus.

MO9845323-AI.  
 PD 15-OCT-1998.  
 PD 06-APR-1998; 98WO-FR00691.  
 PR 24-FEB-1998; 98FR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.  
 PA Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;  
 PI WPI; 1998-583190/49.  
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
 PT human immune deficiency virus of group O

Claim 6; Page 43; 55pp; French.

AA080459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys) derived from the peptides represent variable sequences  
 CC connected around short highly conserved regions. The peptides are  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).

Sequence 22 AA:  
 Query Match 91.3%; Score 116; DB 19; Length 22;  
 Best Local Similarity 86.4%; Pred. No. 2,3e-08;  
 Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCGRGLVCTSYVQNNET 22  
 DB 1 LLSWGCGRGLVCTSYVQNNET 22

RESULT 8  
 AA080465 standard; peptide: 22 AA.  
 AA080465:  
 AA080465:  
 28-JAN-1999 (first entry)  
 Peptide derived from a conserved sequence of group O human HIV.  
 DE Peptide derived from a conserved sequence of group O human HIV.  
 XX Group O human immune deficiency virus; HIV; detection; infection.  
 KM Synthetic.  
 OS Immune deficiency virus.

XX MO9845323-AI.  
 XX 15-OCT-1998.  
 XX 06-APR-1998; 98WO-FR00691.  
 XX 24-FEB-1998; 98FR-0002212.  
 XX 09-APR-1997; 97FR-0004356.  
 XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.  
 PA Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;  
 PI WPI; 1998-583190/49.  
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
 PT human immune deficiency virus of group O

Claim 6; Page 43; 55pp; French.

AA080459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys) derived from the peptides represent variable sequences  
 CC connected around short highly conserved regions. The peptides are  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).

Sequence 22 AA:  
 Query Match 91.3%; Score 116; DB 19; Length 22;  
 Best Local Similarity 90.3%; Pred. No. 2,3e-08;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LLSWGCGRGLVCTSYVQNNET 22  
 DB 1 LLSWGCGRGLVCTSYVQNNET 22

RESULT 9  
 AA080463 standard; peptide: 22 AA.  
 AA080463:  
 AA080463:  
 28-JAN-1999 (first entry)  
 Peptide derived from a conserved sequence of group O human HIV.  
 DE Peptide derived from a conserved sequence of group O human HIV.  
 XX Group O human immune deficiency virus; HIV; detection; infection.  
 KM Synthetic.  
 OS Immune deficiency virus.

MO9845323-AI.  
 PD 15-OCT-1998.  
 PD 06-APR-1998; 98WO-FR00691.  
 PR 24-FEB-1998; 98FR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.  
 PA Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;  
 PI WPI; 1998-583190/49.  
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
 PT human immune deficiency virus of group O

Claim 6; Page 42; 55pp; French.

XX AAM80459-74 represent synthetic peptides (either linear or cyclized by Cys-Cys disulphide bonds). The peptides represent variable sequences connected around short highly conserved sequences present in isolates of group O human immune deficiency virus (HIV). The peptides are useful as immunological reagents for detecting infection by group O human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 90.6%; Score 115; DB 19; Length 22;

Best Local Similarity 86.4%; Pred. No. 3.1e-08;

Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LLSWGCKRGRVLCYTSVONNET 22

DB 1 LLSWGCKRGRVLCYTSVONNET 22

WT 10

0470 AAM80470 standard; peptide; 32 AA.

AC AAM80470;

DE 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic;

OS Immune deficiency virus.

PN MO9845323-A1.

PD 15-OCT-1998.

PE 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

PA (SNP1) PASTEUR SANOFI DIAGNOSTICS SA.

PA Cheneboux DMB, Delagrange JFH, Gabelle SJX, Rieunier FY;

PI WPI; 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by human immune deficiency virus of group O

PS Claim 6; Page 44; 55pp; French.

XX AAM80459-74 represent synthetic peptides (either linear or cyclized by Cys-Cys disulphide bonds). The peptides represent variable sequences connected around short highly conserved sequences present in isolates of group O human immune deficiency virus (HIV). The peptides are useful as immunological reagents for detecting infection by group O human immune deficiency virus (HIV).

XX Sequence 32 AA;

Query Match 89.8%; Score 114; DB 19; Length 32;

Best Local Similarity 86.4%; Pred. No. 6e-08;

Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKRGRVLCYTSVONNET 22

DB 1 LLSWGCKRGRVLCYTSVONNET 32

WT 10

0470 AAM80470 standard; peptide; 32 AA.

AC AAM80470;

DE 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

OS Synthetic;

OS Immune deficiency virus.

AAM80459 standard; peptide; 22 AA.

AAM80459;

DE 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic;

OS Immune deficiency virus.

PN MO9845323-A1.

PD 15-OCT-1998.

PE 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

PA (SNP1) PASTEUR SANOFI DIAGNOSTICS SA.

PA Cheneboux DMB, Delagrange JFH, Gabelle SJX, Rieunier FY;

PI WPI; 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by human immune deficiency virus of group O

PS Claim 6; Page 42; 55pp; French.

XX AAM80459-74 represent synthetic peptides (either linear or cyclized by Cys-Cys disulphide bonds). The peptides represent variable sequences connected around short highly conserved sequences present in isolates of group O human immune deficiency virus (HIV). The peptides are useful as immunological reagents for detecting infection by group O human immune deficiency virus (HIV).

XX Sequence 22 AA;

Query Match 89.8%; Score 113; DB 19; Length 22;

Best Local Similarity 86.4%; Pred. No. 5.7e-08;

Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKRGRVLCYTSVONNET 22

DB 1 LLSWGCKRGRVLCYTSVONNET 22

WT 10

0470 AAM80471 standard; peptide; 32 AA.

AC AAM80471;

DE 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

OS Synthetic;

OS Immune deficiency virus.

PN MO9845323-A1.

PD 15-OCT-1998.

PE 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

PA (SNP1) PASTEUR SANOFI DIAGNOSTICS SA.

PA Cheneboux DMB, Delagrange JFH, Gabelle SJX, Rieunier FY;

PI WPI; 1998-583190/49.

CC	containing the strains AH70 and MP5180. The invention relates to the
CC	discovery of several new strains of HIV-1 which can be placed in group O,
CC	based on the partial sequences of the C2V3-env, gp41 and gag genes (see
CC	AH49470/-39 and AA007339-66). The novel strains have been deposited as
CC	recombinants GCRK-13501 (BCR02), BCB501 (BCEP), BCST133 (BCST),
CC	BCT07 (BCT07) and BCPOL (BCEP) at the European Patent Office (EPO).
CC	The present invention is from the strain BCP13 and corresponds to a fragment of
CC	the gp41 protein encoded by the env gene. The nucleic acids can be used
CC	to detect gp. O HIV-1 strains by hybridisation or (as primers) by gene
CC	amplification, also for screening and typing of such strains. Peptides
CC	encoded by the nucleic acids can be used as immunogens to raise Ab for
CC	detecting gp. O HIV-1.
CC	
SC	
SO	Sequence 40 AA:
Query Match	96.6%; Score 110; DB 17; Length 40;
Beat Local Similarity	81.8%; Pred.No. 2,4e-07;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	
Oy	1 LLSMGRGRLVCTYSVNNET 22       Db 19 LLSMGRGRLVCTYSVNMT 40
RESULT 14	
AA05565	AA05565 standard; Protein: 113 AA.
XX	AA05565;
DT	19-JUL-1999 (first entry)
XX	
DE	HIV-1 group O isolate MP539-PBMC SP41 antigen.
XX	
KW	HIV-1-group O; Outlier strains; gp41; envelope protein; antigen;
XX	vaccine; diagnosis; AIDS.
OS	Human immunodeficiency virus type 1.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 65
FT	Misc-difference 74 /note="encoded by AMW"
FT	Misc-difference 74 /note="encoded by ATR"
FT	Misc-difference 80 /note="encoded by GAK"
FT	Misc-difference 86
FT	/note="encoded by AGY"
XX	
XX	MO9904011-AZ.
XX	
XX	28-JAN-1999.
XX	
Pf	20-JUL-1998; 98NC-BP04522.
PR	18-JUL-1997; 97EP-0870110.
XX	
XX	(INNO-) INNOCENTIS NV.
XX	
XX	Delaporte E, Peeters M, Saman E, Vanden Haesevelde M,
DR	WPI, 1999-132255/11.
XX	N-PDB; AA05565.
PT	New isolated HIV-1 group O strains - used to produce
PT	polynucleotides, antigens and antibodies for use in diagnosis and in
PT	vaccines for prevention of HIV-1 infection
XX	
XX	Claim 3; Fig 6; 16pp; English.
CC	
CC	The present sequence is an antigen of the gp41 protein of HIV-1
CC	group O (Outlier) strain MP539-PBMC, a Cameroon isolate. The
CC	invention relates to new HIV-1 group O antigens (see AA05565-625).

CC and the use of these antigens, or nucleic acids encoding them (see  
CC Xiang et al., 1990). In the diagnosis and prophylaxis of AIDS, they can be  
CC used as antigens for the development of diagnostic assays and for  
CC the development of vaccines. HIV-1 group O infection, and for  
CC differentiating different types of HIV-1 group O infection, in  
CC Vaccines that provide protective immunity against HIV-1 infection, in  
CC particular against HIV-1 group O infection, comprise at least one  
CC HIV-1 type O antigen, a nucleic acid encoding such an antigen, a  
CC virus-like particle comprising such an antigen, or an attenuated  
CC form of an HIV-1 type O strain. The invention also relates to new  
CC group O strains, mostly from patients from Cameroon and its  
CC neighboring countries.

SO Sequence 113 AA;

Query Match 86.6%; Score 110; DB 20; Length 113;  
Best Local Similarity 77.3%; Pred. No. 6.2e-07;  
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0.

1 LLSMGGCRGRGLVCYTSVQNMNET 22  
||:||||:||||:||||:||||:  
39 LILMGGCKRRLICVTSVQNMNT 60

RESULT 15  
AAV77373  
XX AAV77373 standard, Protein: 200 AA.  
XX  
XX AAV77373;  
XX  
XX 22-MAY-2000 (first entry)  
XX  
XX HIV-1 group O env gp120/gp41 pCO-5 recombinant protein, SRQ ID NO:56.  
XX  
XX HIV-1 group O, env; gp120; gp41; glycoprotein; monoclonal antibody;  
XX immunosay; positive control; affinity purification; therapeutic;  
XX Escherichia coli; antigen; synthetic gene construction; mutain;  
XX deletion mutation.  
XX  
XX Human immunodeficiency virus type 1 group O isolate HAM112.  
XX Synthetic.  
XX  
XX WO200004383-A2.  
XX  
XX 27-JAN-2000.  
XX  
XX 09-JUL-1999; 99MO-US15469.  
XX  
XX 14-JUL-1998; 98US-0115171.  
XX  
XX (ABBO ) ARBOTT LAB.  
XX  
XX Scheffell JW, Hackett JR, Tyner JD, Hickman RK;  
XX WPI: 2000-171290/15.  
XX N-PSDB; AA290284.  
XX  
XX Novel monoclonal antibodies useful as positive control reagent for  
XX detecting human immunodeficiency virus infections and diagnosing,  
XX evaluating or prognosing viral disease -  
XX  
XX Example 3; Fig 9; 148pp; English.  
XX  
XX The invention relates to anti-HIV-1 group O monoclonal antibodies, which  
XX may be used as positive control reagents in immunoassays to detect and  
XX identify HIV-1 group O infection. The invention also comprises a  
XX monoclonal antibody which binds specifically to an HIV-1 group O  
XX antigen, which has no more than 15% cross reactivity to a corresponding  
XX antigen selected from HIV-1 group M antigens and HIV-2 antigens; and a  
XX method of using a monoclonal antibody as a positive control reagent in  
XX an immunoassay for the detection of anti HIV-1 group O antibodies. The  
XX monoclonal antibodies are useful as positive control reagents in  
XX immunoassays capable of detecting anti-HIV-1 group O antibodies. Such  
XX immunoassays involve coupling a monoclonal antibody with HIV group-1

CC antigen and detecting the antigen-antibody complex. The monoclonal  
CC antibodies of the invention would be used to ensure that the reagents  
CC monoclonal antibodies may also can be immobilized on a matrix and used  
CC for affinity purification of specific HIV-1 group O-derived proteins  
CC from cell cultures or biological tissues. The monoclonal antibodies can  
CC also be used for generating chimeric antibodies for therapeutic use.  
CC Different epitopes of HIV antigens can be used in combination in assay to  
CC diagnose, evaluate, or prognosticate HIV disease condition. The group O  
CC antigens from HIV-1 group M and HIV-2 antigens. Sequences AAV77369-77375  
CC genes AA290280-290286. The recombinant HIV-1 env proteins contain  
CC various deletions relative to the native HAM112 isolate env protein  
CC (AAV77376). The recombinant HIV-1 group O antigens were purified and used  
CC to screen hybridoma cultures.

SO Sequence 200 AA;

Query Match 86.6%; Score 110; DB 21; Length 200;  
Best Local Similarity 77.3%; Pred. No. 1e-06;  
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0.

1 LLSMGGCRGRGLVCYTSVQNMNET 22  
||:||||:||||:||||:||||:  
112 LILMGGCKRRLICVTSVQNMNT 133

DB 112 LILMGGCKRRLICVTSVQNMNT 133

Search completed: May 29, 2003, 10:36:22  
Job time : 30.333 secs

**THIS PAGE BLANK (USPTO)**

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:36 ; Search time 9.95238 Seconds

(without alignments)  
65,040 Million cell updates/sec.

Title: US-09-147-362a-8

Perfect score: 127

Sequence: 1 LLSWGCGRJLVCTSYVQNNR 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: Issued Patents AA:  
1: /cgn2\_5/pdata/1/isa/SA COMB pep.\*  
2: /cgn2\_5/pdata/1/isa/58 COMB pep.\*  
3: /cgn2\_5/pdata/1/isa/68 COMB pep.\*  
4: /cgn2\_5/pdata/1/isa/68 COMB pep.\*  
5: /cgn2\_5/pdata/1/isa/PC/US COMB pep.\*  
6: /cgn2\_5/pdata/1/isa/PC/US COMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	92.1	40	US-08-894-699-39	Sequence 39, App1
2	117	92.1	40	US-08-894-699-39	Sequence 39, App1
3	110	86.6	40	US-08-894-699-39	Sequence 39, App1
4	110	86.6	40	US-08-894-699-39	Sequence 39, App1
5	110	86.6	40	US-08-894-699-39	Sequence 39, App1
6	110	86.6	40	US-08-894-699-39	Sequence 39, App1
7	110	86.6	40	US-08-894-699-39	Sequence 39, App1
8	110	86.6	40	US-08-894-699-39	Sequence 39, App1
9	110	86.6	40	US-08-894-699-39	Sequence 39, App1
10	110	86.6	40	US-08-894-699-39	Sequence 39, App1
11	110	86.6	40	US-08-894-699-39	Sequence 39, App1
12	110	86.6	40	US-08-894-699-39	Sequence 39, App1
13	110	86.6	40	US-08-894-699-39	Sequence 39, App1
14	110	86.6	40	US-08-894-699-39	Sequence 39, App1
15	110	86.6	40	US-08-894-699-39	Sequence 39, App1
16	110	86.6	40	US-08-894-699-39	Sequence 39, App1
17	110	86.6	40	US-08-894-699-39	Sequence 39, App1
18	110	86.6	40	US-08-894-699-39	Sequence 39, App1
19	110	86.6	40	US-08-894-699-39	Sequence 39, App1
20	110	86.6	40	US-08-894-699-39	Sequence 39, App1
21	110	86.6	40	US-08-894-699-39	Sequence 39, App1
22	110	86.6	40	US-08-894-699-39	Sequence 39, App1
23	110	86.6	40	US-08-894-699-39	Sequence 39, App1
24	110	86.6	40	US-08-894-699-39	Sequence 39, App1
25	110	86.6	40	US-08-894-699-39	Sequence 39, App1
26	110	86.6	40	US-08-894-699-39	Sequence 39, App1
27	110	86.6	40	US-08-894-699-39	Sequence 39, App1

28	104	81.9	33	US-08-433-428D-8	Sequence 8, App1
29	104	81.9	40	US-08-894-699-41	Sequence 41, App1
30	104	81.9	40	US-08-894-699-41	Sequence 41, App1
31	104	81.9	40	US-08-894-699-41	Sequence 41, App1
32	104	81.9	40	US-08-894-699-41	Sequence 41, App1
33	103	81.1	40	US-08-894-699-41	Sequence 41, App1
34	103	81.1	40	US-08-894-699-41	Sequence 41, App1
35	102	80.3	40	US-08-894-699-41	Sequence 41, App1
36	102	80.3	40	US-08-894-699-41	Sequence 41, App1
37	101	79.5	33	US-08-433-428D-68	Sequence 68, App1
38	101	79.5	33	US-08-433-428D-68	Sequence 68, App1
39	101	79.5	33	US-08-433-428D-68	Sequence 68, App1
40	101	79.5	33	US-08-433-428D-68	Sequence 68, App1
41	101	79.5	33	US-08-433-428D-68	Sequence 68, App1
42	101	79.5	33	US-08-433-428D-68	Sequence 68, App1
43	101	79.5	33	US-08-894-699-66	Sequence 66, App1
44	100	78.7	33	US-08-894-699-66	Sequence 66, App1
45	100	78.7	33	US-08-894-699-66	Sequence 66, App1

## ALIGNMENTS

RESULT 1  
US-08-894-699-39  
Sequence 39, Application US/08894699  
Patent No. 6,030,725  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SEXTON  
APPLICANT: LOUSSETT-ALMA, IBITISSAM  
APPLICANT: LY, THOM-DUONG  
TITLE: CHALK-BANDLER, MARTI-LAURE  
TITLE: INVENTION: VIBRATED, AND USES THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: OELON, SPYVAK, MCLELLAND, MAIER & NEUSTADT,  
STREET: 1155 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
SOFTWARE: PC DOS/MS-DOS  
CURRENT APPLICATION DATA: case #1.0, Version #1.30  
APPLICATION NUMBER: 01-DEC-1997  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 1/CT/FR96/00294  
PRIORITY APPLICATION DATA: 1996  
APPLICATION NUMBER: PR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OELON, NORMAN F.  
REGISTRATION NUMBER: 24, 614  
TELEPHONE: 703-413-2220  
TELEFAX: 703-413-2220  
TELEPHONE: 703-413-2220  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acids  
SUBSTRATE: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-09-894-699-39

Query Match 92.1%; Score 117; DB 3; Length 40;  
Best Local Similarity 86.4%; Pred. No. 1.7e-10;  
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1 L15SGGCRRLVCTYSVNNMT 22  
DB 19 L15SGGCRRLVCTYSVNNMT 40

## RESULT 2

US-09-444-410-39

Sequence 68; Application US/09444410

Patent No. 6270975

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS

APPLICANT: SARAGOSTI, SEVIBO

APPLICANT: LOUSSERT-AJAKA, IBITISSAM

APPLICANT: LY, THOI-DIONG, MARIE-LAURE

TITLE OF INVENTION: VIRUSES, AND USES THEREOF

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSER: P.C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/444,410

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

FILING DATE: NUMBER: 08/894,699

PRIOR APPLICATION NUMBER: PR 95/02236

FILING DATE: 27-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REFERENCE/DOCKET NUMBER: 0354-0020-OPCT

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

TYPE: amino acids

STANDARDS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-444-410-39

Query Match 92.1%; Score 117; DB 4; Length 40;

Best Local Similarity 86.4%; Pred. No. 1.7e-10;

Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1 L15SGGCRRLVCTYSVNNMT 22

DB 19 L15SGGCRRLVCTYSVNNMT 40

RESULT 3  
US-09-894-699-68

Sequence 68; Application US/08946999

Patent No. 6030769

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS

APPLICANT: SARAGOSTI, SEVIBO

APPLICANT: LOUSSERT-AJAKA, IBITISSAM

APPLICANT: LY, THOI-DIONG, MARIE-LAURE

TITLE OF INVENTION: VIRUSES, AND USES THEREOF

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSER: P.C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/00294

FILING DATE: 26-FEB-1996

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: PR 95/02236

FILING DATE: 27-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REFERENCE/DOCKET NUMBER: 0354-0020-OPCT

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:

TYPE: amino acids

STANDARDS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-894-699-68

Query Match 86.6%; Score 110; DB 3; Length 40;

Best Local Similarity 81.8%; Pred. No. 1.7e-09;

Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 L15SGGCRRLVCTYSVNNMT 22

DB 19 L15SGGCRRLVCTYSVNNMT 40

RESULT 4

US-09-444-410-69

Sequence 68; Application US/09444410

Patent No. 6030769

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS

APPLICANT: SARAGOSTI, SEVIBO

APPLICANT: LOUSSERT-AJAKA, IBITISSAM

APPLICANT: LY, THOI-DIONG, MARIE-LAURE

TITLE OF INVENTION: VIRUSES, AND USES THEREOF

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSER: P.C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk



TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 NUMBER OF SEQUENCES: 61  
 CORRESPONDENCE ADDRESS: 61  
 ADDRESSER: P. C.  
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202-4302  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/444,410  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/894,699  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 1995-08-15  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-3200  
 INFORMATION FOR SEQ ID NO: 68:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 40 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-444-410-68  
 Query Match 86.6%; Score 110; DB 4; Length 40;  
 Best Local Similarity 81.8%; Pred. No. 1,7e-09;  
 Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 1 LLSMCGCRRLICITYSYVNMET 22  
 19 LLSMCGCRRLICITYSYVNMET 40  
 RESULT 5  
 US-08-912-129A-58  
 Sequence 58, Application US/08912129A  
 Patent No. 5925533  
 GENERAL INFORMATION:  
 APPLICANT: HACKETT, JOHN JR.  
 APPLICANT: HICKMAN, ROBERT K.  
 APPLICANT: VARTKE, VINCENT A. JR.  
 APPLICANT: NECKLAMS, ELIZABETH A.  
 APPLICANT: BRENNAN, ALAN M.  
 APPLICANT: GOLDBERG, CATHARINE A.  
 APPLICANT: DEVARE, SUSHIL G.  
 TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION  
 NUMBER OF SEQUENCES: 89  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Abbott Laboratories  
 STREET: 100 Abbott Park Road  
 CITY: Abbott Park  
 STATE: IL  
 COUNTRY: USA

ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: MS-DOS (Windows 95)  
 SOFTWARE: Microsoft Word (ASCII format output)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/912,129A  
 FILING DATE: 15-AUG-1997  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Danckerts, Andreas M.  
 REGISTRATION NUMBER: 32,652  
 REFERENCE/DOCKET NUMBER: 6109, US .01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 847-917-9803  
 TELEFAX: 847-938-2623  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 58:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 215 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-912-129A-58  
 Query Match 86.6%; Score 110; DB 2; Length 215;  
 Best Local Similarity 77.3%; Pred. No. 9.9e-09;  
 Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 1 LLSMCGCRRLICITYSYVNMET 22  
 127 LLSMCGCRRLICITYSYVNMET 148  
 RESULT 6  
 US-08-912-129A-48  
 Sequence 48, Application US/08912129A  
 Patent No. 5925533  
 GENERAL INFORMATION:  
 APPLICANT: VALLANI, ANNARUZELA S.  
 APPLICANT: HACKETT, JOHN JR.  
 APPLICANT: HICKMAN, ROBERT K.  
 APPLICANT: VARTKE, VINCENT A. JR.  
 APPLICANT: NECKLAMS, ELIZABETH A.  
 APPLICANT: BRENNAN, ALAN M.  
 APPLICANT: GOLDBERG, CATHARINE A.  
 APPLICANT: DEVARE, SUSHIL G.  
 TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION  
 NUMBER OF SEQUENCES: 89  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Abbott Laboratories  
 STREET: 100 Abbott Park Road  
 CITY: Abbott Park  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: MS-DOS (Windows 95)  
 SOFTWARE: Microsoft Word (ASCII format output)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/912,129A  
 FILING DATE: 15-AUG-1997  
 CLASSIFICATION: 436  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:

```

NAME: Danckers, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET INFORMATION: 6109 US. 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-129A-48

Query Match      86.6% Score 110; DB 2; Length 245;
Best Local Similarity 77.3%; Pred. No. 1.1e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 LLSMCGCRGLCTYSVMNET 22
|||||:|||||:|||||
127 LLLMCGCRGLCTYSVMNET 148
|||||:|||||:|||||

RESULT 7
US-08-912-129A-52
Sequence 52 Application US/08912129A
Patent No. 592553
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K. JR.
APPLICANT: NECKLMS, VINCENT A. JR.
APPLICANT: NICKLMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARIE, SUSHLI G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS: Abbott Laboratories
CITY: Abbott Park Road
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 173 amino acids
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-129A-60

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MOLECULE TYPE: protein
US-08-912-129A-52

Query Match      86.6% Score 110; DB 2; Length 373;
Best Local Similarity 77.3%; Pred. No. 1.7e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 LLSMCGCRGLCTYSVMNET 22
|||||:|||||:|||||
127 LLLMCGCRGLCTYSVMNET 148
|||||:|||||:|||||

RESULT 8
US-08-912-129A-60
Sequence 60 Application US/08912129A
Patent No. 592553
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K. JR.
APPLICANT: NECKLMS, VINCENT A. JR.
APPLICANT: NICKLMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARIE, SUSHLI G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
CITY: Abbott Laboratories
CITY: Abbott Park Road
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-912-129A-60

Query Match      86.6% Score 110; DB 2; Length 460;
Best Local Similarity 77.3%; Pred. No. 2.2e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 LLSMCGCRGLCTYSVMNET 22
|||||:|||||:|||||
372 LLLMCGCRGLCTYSVMNET 393
|||||:|||||:|||||

RESULT 9

```

```

US-08-912-129A-50
; Sequence 50, Application US/08912129A
; Patent No. 5922533
; GENERAL INFORMATION:
; APPLICANT: VALLARI, ANDRUEZLA S.
; APPLICANT: HACKETT, JOHN JR.
; APPLICANT: HICKMAN, ROBERT K.
; APPLICANT: VARTERK, VINCENT A. JR.
; APPLICANT: NECKLAMS, ELIZABETH A.
; APPLICANT: GOLDEN, ALAN M.
; APPLICANT: BRENNAN, CATHERINE A.
; APPLICANT: DEWARE, SUSHIL G.
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; STREET: 100 Abbott Park Road
; City: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
; OPERATING SYSTEM: MS-DOS (Windows 95)
; SOFTWARE: Microsoft Word (ASCII format output)
; CURRENT APPLICATION DATA:
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Danckers, Andreas M.
; REGISTRATION NUMBER: 32,652
; REFERENCE/DOCKET NUMBER: 6109, US .01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-9803
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 490 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; 8-912-129A-50
Query Match 96.6%; Score 110; DB 2; Length 490;
Best Local Similarity 77.3%; Pred. No. 2,3e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Cy 1 LLSWGCGRGLICVTSVKNMET 22
Db 372 LLLNMGCKRGLICVTSVKNMET 393
RESULT 10
US-08-912-129A-54
; Sequence 54, Application US/08912129A
; Patent No. 5922533
; GENERAL INFORMATION:
; APPLICANT: VALLARI, ANDRUEZLA S.
; APPLICANT: HACKETT, JOHN JR.
; APPLICANT: HICKMAN, ROBERT K.
; APPLICANT: VARTERK, VINCENT A. JR.
; APPLICANT: NECKLAMS, ELIZABETH A.
; APPLICANT: GOLDEN, ALAN M.
; APPLICANT: BRENNAN, CATHERINE A.
; APPLICANT: DEWARE, SUSHIL G.
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; STREET: 100 Abbott Park Road
; City: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
; OPERATING SYSTEM: MS-DOS (Windows 95)
; SOFTWARE: Microsoft Word (ASCII format output)
; CURRENT APPLICATION DATA:
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Danckers, Andreas M.
; REGISTRATION NUMBER: 32,652
; REFERENCE/DOCKET NUMBER: 6109, US .01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-9803
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; 8-912-129A-54
Query Match 86.6%; Score 110; DB 2; Length 618;
Best Local Similarity 77.3%; Pred. No. 2,9e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Cy 1 LLSWGCGRGLICVTSVKNMET 22
Db 372 LLLNMGCKRGLICVTSVKNMET 393

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; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; STREET: 100 Abbott Park Road
; City: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
; OPERATING SYSTEM: MS-DOS (Windows 95)
; SOFTWARE: Microsoft Word (ASCII format output)
; CURRENT APPLICATION DATA:
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Danckers, Andreas M.
; REGISTRATION NUMBER: 32,652
; REFERENCE/DOCKET NUMBER: 6109, US .01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-9803
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; 8-912-129A-54
Query Match 86.6%; Score 110; DB 2; Length 618;
Best Local Similarity 77.3%; Pred. No. 2,9e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Cy 1 LLSWGCGRGLICVTSVKNMET 22
Db 372 LLLNMGCKRGLICVTSVKNMET 393
RESULT 11
US-08-912-129A-61
; Sequence 61, Application US/08912129A
; Patent No. 5922533
; GENERAL INFORMATION:
; APPLICANT: VALLARI, ANDRUEZLA S.
; APPLICANT: HACKETT, JOHN JR.
; APPLICANT: HICKMAN, ROBERT K.
; APPLICANT: VARTERK, VINCENT A. JR.
; APPLICANT: NECKLAMS, ELIZABETH A.
; APPLICANT: GOLDEN, ALAN M.
; APPLICANT: BRENNAN, CATHERINE A.
; APPLICANT: DEWARE, SUSHIL G.
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; STREET: 100 Abbott Park Road
; City: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
; OPERATING SYSTEM: MS-DOS (Windows 95)
; SOFTWARE: Microsoft Word (ASCII format output)
; CURRENT APPLICATION DATA:
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Danckers, Andreas M.
; REGISTRATION NUMBER: 32,652
; REFERENCE/DOCKET NUMBER: 6109, US .01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-9803
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; 8-912-129A-61
Query Match 86.6%; Score 110; DB 2; Length 618;
Best Local Similarity 77.3%; Pred. No. 2,9e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Cy 1 LLSWGCGRGLICVTSVKNMET 22
Db 372 LLLNMGCKRGLICVTSVKNMET 393

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CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/912.129A  
 FILING DATE: 15-AUG-1997  
 CLASSIFICATION: 436  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Danchoeva, Andread M.  
 REGISTRATION NUMBER: 32,652  
 REFERENCE/DOCKET NUMBER: 6109 US-01  
 TELEPHONE: 847-938-2603  
 TELEFAX: 847-938-2633  
 TELETYPE:  
 INFORMATION FOR SEQ ID NO: 61:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 873 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein  
 US-08-912-129A-61

Query Match 86.6%; Score 110; DB 2; Length 873;  
 Best Local Similarity 77.3%; Pred. No. 4.2e-08;  
 Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 LLSMCGCRRLVCTSYVMNET 22  
 Db 601 LLMWGCKRRLVCTSYVMNET 622

RESULT 12  
 US-08-817-441-94  
 Sequence 94, Application US/08817441  
 Patent No. 6399294  
 GENERAL INFORMATION:  
 APPLICANT: CHARNEAU, PIERRE  
 APPLICANT: CLAVEL, FRANCOISE  
 APPLICANT: COHEN, JACQUES  
 APPLICANT: GUILLET, CAROLINE  
 APPLICANT: GUETARD, DENISE  
 APPLICANT: MONTAGNIER, LUC  
 APPLICANT: DONON DE SAINT-MARTIN, JACQUELINE  
 APPLICANT: COHEN, JACQUES  
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR  
 TITLE OF INVENTION: SUBTYPE) ANTIGENS  
 NUMBER OF SEQUENCES: 103  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Plimagan, Henderson, Farbow, Garrett &  
 ADDRESSEE: Dunner, L.L.P.  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/817.441  
 FILING DATE: 11-JUL-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/FR 95/01391  
 FILING DATE: 20-OCT-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 9412554  
 FILING DATE: 20-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 9502526

FILING DATE: 03-MAR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 03260.6005-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 INFORMATION FOR SEQ ID NO: 94:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 37 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-817-441-94

Query Match 85.8%; Score 109; DB 4; Length 37;  
 Best Local Similarity 77.3%; Pred. No. 2.2e-09;  
 Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

1 LLSMCGCRRLVCTSYVMNET 22  
 Db 14 LLMWGCKRRLVCTSYVMNET 35

RESULT 13  
 US-08-817-441-100  
 Sequence 100, Application US/08817441  
 Patent No. 6399294  
 GENERAL INFORMATION:  
 APPLICANT: CHARNEAU, PIERRE  
 APPLICANT: CLAVEL, FRANCOISE  
 APPLICANT: COHEN, JACQUES  
 APPLICANT: GUILLET, CAROLINE  
 APPLICANT: GUETARD, DENISE  
 APPLICANT: MONTAGNIER, LUC  
 APPLICANT: DONON DE SAINT-MARTIN, JACQUELINE  
 APPLICANT: COHEN, JACQUES  
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR  
 TITLE OF INVENTION: SUBTYPE) ANTIGENS  
 NUMBER OF SEQUENCES: 103  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Plimagan, Henderson, Farbow, Garrett &  
 ADDRESSEE: Dunner, L.L.P.  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/817.441  
 FILING DATE: 11-JUL-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/FR 95/01391  
 FILING DATE: 20-OCT-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 9412554  
 FILING DATE: 20-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 9502526  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 03260.6005-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000

Search completed: May 29, 2003, 10:41:28  
 Job time : 9.95238 secs

TRIPLEX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 100:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 104 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 M-08-817-441-100  
 MOLECULE TYPE: peptide

Query Match  
 Best Local Similarity 85.8%; Score 109; DB 4; Length 104;  
 Best Local Similarity 77.3%; Pred. No. 6,5e-09;

Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSWCGCRGLVCTYSVQNNET 22  
 DB 45 LLSWCGCRGLVCTYSVQNNET 66

SEQUENCE 6, Application US/09433428D  
 Patent No. 6149910  
 GENERAL INFORMATION:  
 APPLICANT: De Lays, Robert J.  
 APPLICANT: 2004/11/14

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O

FILE REFERENCE: CDS-207

CURRENT APPLICATION NUMBER: US/09/433,428D

CURRENT FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 6

LENGTH: 33

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-433-428D-6

Query Match  
 Best Local Similarity 85.0%; Score 108; DB 4; Length 33;  
 Best Local Similarity 85.0%; Pred. No. 2.8e-09;  
 Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWCGCRGLVCTYSVQNN 20  
 DB 14 LLSWCGCRGLVCTYSVQNN 33

SEQUENCE 25, Application US/09433428D  
 Patent No. 6149910  
 GENERAL INFORMATION:  
 APPLICANT: De Lays, Robert J.  
 APPLICANT: 2004/11/14

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O

FILE REFERENCE: CDS-207

CURRENT APPLICATION NUMBER: US/09/433,428D

CURRENT FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 25

LENGTH: 33

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-433-428D-25

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 Best Local Similarity 84.3%; Score 107; DB 4; Length 33;  
 Best Local Similarity 85.0%; Pred. No. 3.9e-09;

Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLSWCGCRGLVCTYSVQNN 20  
 DB 14 LLSWCGCRGLVCTYSVQNN 33

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GenCore version 5.1.6  
Copyright (C) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 29, 2003, 10:39:21 Search time 19.0317 Seconds

(Without alignments)  
117.011 Million cell updates/sec

Title: US-09-147-362a-8

Perfect score: 127

Sequence: 1 LLSMNGRGLVCTSYVNMET 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 385519 seqs, 101223694 residues

1 number of hits satisfying chosen parameters: 385519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter: 45 summaries

Published Applications AA:\*

- 1: /cgn2\_6/p/codata/2/pub/paa/US08\_NEW\_PUB.pep:\*
- 2: /cgn2\_6/p/codata/2/pub/paa/PC1\_NEM\_PUB.pep:\*
- 3: /cgn2\_6/p/codata/2/pub/paa/US06\_NEM\_PUB.pep:\*
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- 8: /cgn2\_6/p/codata/2/pub/paa/US09\_PUBCOMB.pep:\*
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- 12: /cgn2\_6/p/codata/2/pub/paa/US10\_PUBCOMB.pep:\*
- 13: /cgn2\_6/p/codata/2/pub/paa/US60\_NEM\_PUB.pep:\*
- 14: /cgn2\_6/p/codata/2/pub/paa/US60\_PUBCOMB.pep:\*

SUMMARIES

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2	110	86.6	245	1	US-08-911-824-48
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4	110	86.6	373	1	US-08-911-824-50
5	110	86.6	460	1	US-08-911-824-60
6	110	86.6	488	1	US-08-911-824-95
7	110	86.6	490	1	US-08-911-824-50
8	110	86.6	526	1	US-08-911-824-97
9	110	86.6	618	1	US-08-911-824-54
10	110	86.6	706	1	US-08-911-824-51
11	110	86.6	706	1	US-08-911-824-51
12	110	86.6	873	1	US-08-911-824-61
13	109	85.8	37	9	US-10-026-741-94
14	109	85.8	104	9	US-10-026-741-100
15	109	85.8	37	9	US-10-026-741-86
16	106	83.5	220	10	US-09-854-816-104
17	105	82.7	32	9	US-10-026-741-30
18	105	82.7	32	9	US-10-026-741-101
19	100	78.7	37	3	US-10-026-741-7

20	100	78.7	37	9	US-10-026-741-80	Sequence 90, App1
21	100	78.7	351	9	US-10-026-741-47	Sequence 47, App1
22	100	78.7	877	9	US-10-026-741-102	Sequence 102, App1
23	99	78.0	24	9	US-10-026-741-34	Sequence 34, App1
24	98	77.2	37	9	US-10-026-741-88	Sequence 88, App1
25	96	75.6	213	10	US-09-854-816-103	Sequence 103, App1
26	93	73.2	23	9	US-09-886-847-4	Sequence 4, App1
27	93	73.2	23	12	US-10-000-321-2	Sequence 2, App1
28	93	73.2	35	9	US-09-886-155-62	Sequence 62, App1
29	93	73.2	35	9	US-09-886-155-46	Sequence 46, App1
30	93	73.2	35	9	US-09-886-149-62	Sequence 62, App1
31	93	73.2	35	9	US-09-886-159-62	Sequence 62, App1
32	93	73.2	146	12	US-10-000-321-105	Sequence 105, App1
33	93	73.2	204	10	US-09-854-816-106	Sequence 106, App1
34	93	73.2	351	9	US-09-886-155-46	Sequence 46, App1
35	93	73.2	351	9	US-09-886-155-46	Sequence 46, App1
36	85	66.9	268	10	US-09-854-816-39	Sequence 39, App1
37	83	65.4	37	9	US-10-026-741-84	Sequence 84, App1
38	83	65.4	204	10	US-09-854-816-106	Sequence 106, App1
39	83	65.4	1231	9	US-10-055-271-94	Sequence 94, App1
40	83	65.4	22	9	US-10-055-271-81	Sequence 81, App1
41	82	64.6	198	10	US-09-854-816-81	Sequence 81, App1
42	81	63.8	198	10	US-10-026-741-82	Sequence 82, App1
43	80	63.0	126	10	US-09-854-816-77	Sequence 77, App1
44	80	63.0	126	10	US-09-854-816-77	Sequence 77, App1
45	80	63.0	126	10	US-09-854-816-77	Sequence 77, App1

ALIGNMENTS

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RESULT 1
US-08-911-824-58
Sequence 58
US-08-911-824-58
GENERAL INFORMATION: Application US/08911824
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Smith, Robert K.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Shaili G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165.US.OI
CURRENT FILING DATE: 1997-08-15
SOFTWARE: SEQ ID NO 58
SEQ ID NO 58
SEQ ID NO 58
LENGTH: 215
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-8P.
US-08-911-824-58
Query Match 86.6%; Score 110; DB 1; Length 215;
Best Local Similarity 77.3%; Pred. No. 2.9e-08;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0.
Ov 1 LLSMNGRGLVCTSYVNMET 22
Db 127 LLSMNGRGLVCTSYVNMET 148
RESULT 2
US-08-911-824-48
Sequence 48, Application US/08911824
Publication No. US2003000433A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories

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APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US.O1
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 48
LENGTH: 373
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-9PL
US-08-911-824-48
Query Match
Best Local Similarity 96.6%; Score 110; DB 1; Length 245;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
1 LLSWGGCRGLVCTYSVKNNET 22
Db 127 LNLWGCKGRILCTYSVKNNET 148

RESULT 3
US-08-911-824-120
Sequence 120, Application US/08911824
Publication No. US2003004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US.O1
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 120
LENGTH: 381
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-15PL
US-08-911-824-120
Query Match
Best Local Similarity 86.6%; Score 110; DB 1; Length 281;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
1 LLSWGGCRGLVCTYSVKNNET 22
Db 127 LNLWGCKGRILCTYSVKNNET 148

RESULT 4
US-08-911-824-52
Sequence 52, Application US/08911824
Publication No. US2003004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
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APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US.O1
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 52
LENGTH: 373
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-11PL
US-08-911-824-52
Query Match
Best Local Similarity 86.6%; Score 110; DB 1; Length 373;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
1 LLSWGGCRGLVCTYSVKNNET 22
Db 127 LNLWGCKGRILCTYSVKNNET 148

RESULT 5
US-08-911-824-60
Sequence 60, Application US/08911824
Publication No. US2003004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
APPLICANT: Devare, Sushil G.
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
FILE REFERENCE: 6165 US.O1
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 60
LENGTH: 460
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
FEATURE:
OTHER INFORMATION: Encodes recombinant protein pCO-8CKS
US-08-911-824-60
Query Match
Best Local Similarity 86.6%; Score 110; DB 1; Length 460;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
1 LLSWGGCRGLVCTYSVKNNET 22
Db 372 LNLWGCKGRILCTYSVKNNET 393

RESULT 6
US-08-911-824-95
Sequence 95, Application US/08911824
Publication No. US2003004323A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hackett, John R., Jr.
APPLICANT: Yamaguchi, Julie
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Query Match Similarity    96.8% Score 110 DB 1 Length 736;
Best Local Similarity     97.5% Pred No. 1.e-06;
Matches   17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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Db       618 LLTMWCKKRLCYTSVMNET 639
RESULT 12
US-08-911-824-61
Sequence 61, Application US/08911824
Publication No. US2003000432A1
GENERAL INFORMATION:
APPLICANT: Hockett Laboratories
APPLICANT: Hockett Laboratories Jr.
APPLICANT: YemagnichJulie A.
APPLICANT: Golden, Alan W.
APPLICANT: Brennan, Catherine A.
APPLICANT: Hickman, Robert K.
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US-10-026-741-94

SEQUENCE DESCRIPTION: SEQ ID NO: 94:

MATCHES 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Query Match 85.8%; Score 109; DB 9; Length 37;  
Best Local Similarity 77.3%; Pred. No. 0-7e-09;

CY 1 LHSQWCKGKGLCTVSYQWNET 22  
|||:|||:  
DB 14 LRLNMGCGKGLCTVSYQWNET 35

US-026-741-100

PUBLICATION NO. US20030049604A1

GENERAL INFORMATION:

APPLICANT: CHANEAU, PIERRE  
CLAVEL, FRANCOISE  
BORHAN, ANDREW  
QUILLIENT, CAROLINE  
GUERIN, CHRISTOPHE  
MONTAUDO, JULIE  
DONON DE SAINT-MARTIN, JACQUELINE  
COHEN, JAMES

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR SUBTYPED) ANTIGENS

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:  
ADDRESS: Finguel, Henderson, Fairbow, Garrett &  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/026,741  
FILING DATE: 27-Dec-2001

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/817,441  
FILING DATE: 31-MAR-1998  
APPLICATION NUMBER: PCT/FR 95/01391  
FILING DATE: 20-OCT-1995  
APPLICATION NUMBER: FR 9412554  
FILING DATE: 20-OCT-1994  
APPLICATION NUMBER: FR 9502526  
FILING DATE: 03-MAR-1995

AUTHORS:  
NAME: Meyer, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/Docket NUMBER: 03260.6005-00000

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEX: 202-408-4400

INFORMATION FOR SEQUENCE ALIGNMENT:  
SEQUENCE LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear

```

1      MOLECULE TYPE: peptide
2      SEQUENCE DESCRIPTION: SEQ ID NO: 100:
3
4      US-10-026-741-100
5
6      Query Match          58.8%  Score 109;  DB 9;  Length 104;
7      Best Local Similarity 77.3%  Pred. No. 2e-08;
8      Matches 17;  Conservative 3;  Mismatches 2;  Indels 0;
9
10     1  LLSMOCRGRLACVCTSVQNMET 22
11     |||:|||||:|||||:|||||:
12     DB          45  LLLLMOCRGRLACVCTSVQNMET 66
13
14     RESULT 15
15     US-10-026-741-86
16     Sequence 86, Application US/10026741
17     Publication No. US20030043604A1
18     GENERAL INFORMATION:
19     APPLICANT: CHARRAU, PIERRE
20     INVENTOR: CHARRAU, PIERRE
21     BORNAY, ANDREW
22     OUILLENT, CAROLINE
23     GERARD, DENISE
24     MONTAGNIER, LUC
25     DONON, DE SAINT-MARTIN, JACQUELINE
26     COHEN, JACQUES
27     TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
28     NUMBER OF SEQUENCES: 101
29     CORRESPONDENCE ADDRESSES:
30     ADDRESSEE: Finmeagan, Henderson, Farabow, Garrett &
31     Dunner, L.L.P.
32     STREET: 1300 I Street, N.W.
33     CITY: Washington
34     STATE: DC
35     COUNTRY: USA
36     ZIP: 20005-3115
37
38     COMPUTER READABLE FORM:
39     MEDIUM TYPE: Floppy disk
40     COMPUTER: IBM PC compatible
41     OPERATING SYSTEM: PC-DOS/MS-DOS
42     SOFTWARE: Patentin Release #1.0, Version #1.30
43     CURRENT APPLICATION NUMBER: US/10/026,741
44     FILING DATE: 27-Dec-2001
45
46     PRIOR APPLICATION DATA:
47     APPLICATION NUMBER: US 08/817,441
48     FILING DATE: 31-AUG-1998
49     APPLICATION NUMBER: ECT/FR 95/01391
50     FILING DATE: 20-OCT-1995
51     APPLICATION NUMBER: A412554
52     FILING DATE: 20-OCT-1994
53     APPLICATION NUMBER: FR 9502526
54     FILING DATE: 03-MAR-1995
55
56     ATTORNEY/AGENT INFORMATION:
57     NAME: Meyers, Kenneth J.
58     REGISTRATION NUMBER: 25,146
59     REFERENCE/DOCKET NUMBER: 03260.6005-00000
60     TELEPHONE NUMBER: 202-408-4000
61     TELEFAX: 202-408-4400
62
63     INFORMATION FOR SEQ ID NO: 86:
64     SEQUENCE CHARACTERISTICS:
65     LENGTH: 37 amino acids
66     TYPE: amino acid
67     STRAND: single
68     ORIENTATION: 5' to 3'
69     MOLECULE TYPE: peptide
70     SEQUENCE DESCRIPTION: SEQ ID NO: 86:
71
72     US-10-026-741-86
73
74     Query Match          83.5%  Score 106;  DB 9;  Length 37;
75     Best Local Similarity 77.3%  Pred. No. 2.1e-08;

```

Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLSSMCKGRLVCTSVONNET 22  
 DB 14 LLSSMCKGRLVCTSVONNET 35

Search completed: May 29, 2003, 11:03:57  
 Job time : 19.0317 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comphen Gen Ltd.

OW protein - protein search, using sw model

Run on: May 29, 2003, 10:33:06 / Search time 10.8254 Seconds

(without alignments)  
195,370 Million call updates/sec

Title: US-09-147-362a-8

Sequence: 1 LLSWGCGRGLVCTSYVNNET 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: p121.\*

2: p122.\*

3: p123.\*

4: p124.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	85.8	104	2	GP1 ENV protein -
2	106	83.5	85	2	gag ENV protein -
3	100	78.7	877	2	env protein p
4	83	65.4	854	1	env polypotein p
5	82	64.6	357	2	env protein g
6	82	64.6	357	2	env protein g
7	81	63.8	358	2	env protein g
8	81	63.8	358	2	env protein g
9	80	63.0	443	2	env polypotein p
10	80	63.0	853	2	env polypotein p
11	80	63.0	853	2	env polypotein p
12	79	62.2	357	2	env protein g
13	79	62.2	357	2	env protein g
14	79	62.2	357	2	env protein g
15	79	62.2	357	2	env protein g
16	79	62.2	357	2	env protein g
17	79	62.2	357	2	env protein g
18	79	62.2	357	2	env protein g
19	79	62.2	357	2	env protein g
20	79	62.2	357	2	env protein g
21	79	62.2	357	2	env protein g
22	79	62.2	357	2	env protein g
23	79	62.2	357	2	env protein g
24	79	62.2	357	2	env protein g
25	79	62.2	357	2	env protein g
26	79	62.2	357	2	env protein g
27	79	62.2	357	2	env protein g
28	79	62.2	357	2	env protein g

30	79	62.2	859	1	VCLJMN	env polypotein pr
31	79	62.2	861	1	VCLJMV	env polypotein pr
32	79	62.2	861	1	VCLJMV	env polypotein pr
33	79	62.2	868	1	VCLJH4	env polypotein -
34	78.5	61.8	855	2	A45713	Env transmembrane
35	78	61.4	786	2	S28084	env polypotein -
36	77	60.6	856	1	A44963	env polypotein pr
37	76	59.8	846	1	VCLJND	env polypotein pr
38	74.5	58.7	859	1	VCLJND	env polypotein pr
39	74.5	58.7	859	1	VCLJND	env polypotein pr
40	74.5	58.7	859	1	VCLJND	env polypotein pr
41	74.5	58.7	859	1	VCLJND	env polypotein pr
42	73	57.5	729	1	VCLJXK	env polypotein -
43	73	57.5	861	1	VCLJXK	env polypotein pr
44	72.5	57.1	151	2	S30448	env protein - huma
45	72.5	57.1	151	2	S30453	env protein - huma

## ALIGNMENTS

RESULT 1  
S52930 GP1 ENV protein - human immunodeficiency virus type 1 (fragment)

C/Spectra: human immunodeficiency virus type 1, HIV-1, NC\_011595.1, change 26-Aug-1999

C/Spectra: 06-04-952930

C/Spectra: J.H.M., Guehard, D.; Philbert, F.; Chameret, S.; Tabary, T.; Montagner, L.; de

submitted to the EMBL Data Library, January 1995

A/Description: A novel HIV-1 strain illustrates the diversity of the O group.

A/Reference number: S52929

A/Accession: S52930

A/Status: preliminary

A/Notes: genomic RNA

A/Residues: 1-104 (CDR)

A/Cross-references: EMBL:X84328; NID:G695926; PID:CA59066.1; PID:G695927

C/Superfamily: type E retrovirus env polypotein

Query Match 85.8%; Score 109; DB 2; Length 104;  
Best Local Similarity 77.3%; Pred. No. 1.1e-08;  
Matches 17; Conservative 2; Indels 0; Gaps 0;

QY 1 LLSWGCGRGLVCTSYVNNET 22  
DB 45 LLSWGCGRGLVCTSYVNNET 66

RESULT 2  
A53033 GP1 ENV protein - human immunodeficiency virus type 1 (strain Ant70)

C/Spectra: human immunodeficiency virus type 1, HIV-1

C/Spectra: 03-May-1994 #sequence\_revision 03-May-1994 #ext\_change 07-May-1999

C/Accession: A53034

R/Vander Haesevelde, M.; Decourt, J.L.; De Leys, R.J.; Vanderborght, B.; van der Groen,

A/Vitel: genomic cloning and complete sequence analysis of a highly divergent African hu

A/Accession: A53034

A/Status: preliminary

A/Molecule type: genomic RNA

A/Residues: 1-863 <V>N>

A/Cross-references: GB:102587

C/Superfamily: type B retrovirus env polypotein

Query Match 83.5%; Score 106; DB 2; Length 863;  
Best Local Similarity 77.3%; Pred. No. 1.9e-07;  
Matches 17; Conservative 3; Indels 0; Gaps 0;

QY 1 LLSWGCGRGLVCTSYVNNET 22  
DB 594 LLSWGCGRGLVCTSYVNNET 615



C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 12-Apr-1995  
 C/Accession: S22000  
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 Submitted to the EMBL Data Library, July 1991  
 A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by sequence analysis  
 A/Reference number: S22000  
 A/Accession: M22000  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-358 <STR>  
 A/Cross-references: EMBL:X61351  
 C/Suprafamily: type B retrovirus env polypeptide

Query Match 63.8%; Score 81; DB 2; Length 358;  
 Best Local Similarity 65.0%; Pred. No. 0.00055;  
 Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

1 LLSMCGCRGLVCTVYVNN 20  
 94 LGLWCGSGRLCTTVYVNN 113

RESULT 8  
 S70417  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)  
 C/Species: human immunodeficiency virus type 1, HIV-1  
 C/Date: 10-Feb-1993 #sequence\_revision 25-Apr-1997 #text\_change 26-Aug-1999  
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 9, 53-59, 1992  
 A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
 A/Reference number: S70417; PMID:92144209; PMID:1736940  
 A/Accession: S70417  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-358 <STR>  
 A/Cross-references: EMBL:X61351; NID:960184; PIDN:CAA43614.1; PID:960185  
 C/Suprafamily: type B retrovirus env polypeptide

Query Match 63.8%; Score 81; DB 2; Length 358;  
 Best Local Similarity 65.0%; Pred. No. 0.00035;  
 Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

1 LLSMCGCRGLVCTVYVNN 20  
 94 LGLWCGSGRLCTTVYVNN 113

RESULT 9  
 S70417  
 env polypeptide P - human immunodeficiency virus type 1 (fragment)  
 N/Alternate names: coat polypeptide  
 N/Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
 C/Species: human immunodeficiency virus type 1, HIV-1  
 C/Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
 A/Note: host Homo sapiens (man)  
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 AIDS Res. Hum. Retroviruses 9, 53-59, 1992  
 A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
 A/Reference number: M41621; PMID:92107924; PMID:1763038  
 A/Accession: C41621  
 A/Molecule type: DNA  
 A/Residues: 1-358 <STR>  
 A/Cross-references: GB:M77230; NID:9328631; PIDN:AA03792.1; PID:9555015  
 A/Note: this virus was isolated from the mother's sexual partner  
 C/Genetics:  
 A/Gene: env  
 C/Suprafamily: type B retrovirus env polypeptide  
 C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide; protein; coat protein gp41 (fragment) #status predicted <GP2>  
 F/252-443/Domain: coat protein gp41 (fragment) #status predicted <GP2>

F/424-443/Domain: transmembrane #status predicted <TM>  
 F/9,23,36,48,70,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 63.0%; Score 90; DB 2; Length 443;  
 Best Local Similarity 54.5%; Pred. No. 0.00058;  
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LLSMCGCRGLVCTVYVNN 22  
 332 LGLWCGSGRLCTTVYVNN 353

RESULT 10  
 S54384  
 envelope polypeptide - human immunodeficiency virus type 1  
 C/Species: human immunodeficiency virus type 1, HIV-1  
 C/Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999  
 R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 AIDS Res. Hum. Retroviruses 9, 53-59, 1992  
 A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
 A/Reference number: S54377  
 A/Accession: S54384  
 A/Status: preliminary  
 A/Molecule type: genomic RNA  
 A/Residues: 1-853 <TR>  
 A/Cross-references: EMBL:M26519; NID:9329177; PIDN:AAA45370.1; PID:9323365  
 C/Keywords: polypeptide  
 C/Keywords: polypeptide

Query Match 63.0%; Score 90; DB 2; Length 853;  
 Best Local Similarity 54.5%; Pred. No. 0.001;  
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LLSMCGCRGLVCTVYVNN 22  
 589 LGLWCGSGRLCTTVYVNN 610

RESULT 11  
 VJ0248  
 env polypeptide precursor - human immunodeficiency virus Zr-6  
 N/Alternate names: coat polypeptide  
 C/Species: human immunodeficiency virus Zr-6  
 C/Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 15-Jul-1999  
 C/Accession: D26132  
 R/Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Peorino, P.; Schochetman, G.; Cu  
 Gene 52, 71-82, 1987  
 A/Title: Molecular characterization of human immunodeficiency virus from zaire: nucleotide sequence of the env gene  
 A/Reference number: M26132; NID:87248097; PMID:3036660  
 A/Accession: D26132  
 A/Molecule type: DNA  
 A/Residues: 1-855 <STR>  
 A/Cross-references: GB:M3458; GB:M16321; NID:9329398; PIDN:AAA45380.1; PID:9329403  
 A/Note: this virus was isolated from the mother's sexual partner  
 C/Genetics:  
 A/Gene: env  
 C/Suprafamily: type B retrovirus env polypeptide  
 C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide; protein; coat protein gp41 (fragment) #status predicted <GP2>  
 F/20-853/Product: env polypeptide #status predicted <TM>  
 F/20-853/Product: exterior membrane glycoprotein #status predicted <EXTR>  
 F/501-855/Product: transmembrane glycoprotein #status predicted <TM>  
 F/87,129,140,145,158,168,189,199,236,243,264,270,281,297,331,340,355,366,392,398,404

Query Match 63.0%; Score 80; DB 1; Length 855;  
 Best Local Similarity 54.5%; Pred. No. 0.001;  
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LLSMCGCRGLVCTVYVNN 22  
 591 LGLWCGSGRLCTTVYVNN 612

RESULT 12

522006  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 41)  
 C|Species: human immunodeficiency virus type 1, HIV-1  
 C|Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 A|Accession: S22004, S22006  
 A|Cross-references: EMBL:X61353; NID:G60189; PID:CAA43618.1; PID:G60189  
 A|Residues: 1-357 <STE2>  
 A|Molecule type: DNA  
 A|Notes: submitted to the EMBL Data Library, July 1991  
 A|Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR  
 A|Reference number: S70417; MUID:92144209; PMID:1736940  
 A|Accession: S70420  
 A|Status: preliminary  
 A|Molecule type: DNA  
 A|Residues: 1-357 <STE2>  
 A|Cross-references: EMBL:X61354; NID:G60190; PID:CAA43620.1; PID:G60191  
 A|Notes: submitted to the EMBL Data Library, July 1991  
 A|Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR  
 A|Reference number: S70417; MUID:92144209; PMID:1736940  
 C|Superfamily: type E retrovirus env polypeptide

Query Match 62.2%; Score 79; DB 2; Length 357;  
 BL local similarity 60.0%; Pred. No. 0.00067;  
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

DB 93 LIGMCSGKLLCTTAVPNN 112

## RESULT 13

521994  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 271)  
 C|Species: human immunodeficiency virus type 1, HIV-1  
 C|Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 A|Accession: S21994, S70421  
 A|Cross-references: EMBL:X61355; NID:G60179; PID:CAA43622.1; PID:G60180  
 A|Residues: 1-357 <STE2>  
 A|Molecule type: DNA  
 A|Notes: submitted to the EMBL Data Library, July 1991  
 A|Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR  
 A|Reference number: S70417; MUID:92144209; PMID:1736940  
 A|Accession: S21994  
 A|Status: preliminary  
 A|Molecule type: DNA  
 A|Residues: 1-357 <STE2>  
 A|Cross-references: EMBL:X61355; NID:G60179; PID:CAA43622.1; PID:G60180  
 A|Notes: submitted to the EMBL Data Library, July 1991  
 A|Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR  
 A|Reference number: S70417; MUID:92144209; PMID:1736940  
 A|Accession: S70421  
 A|Status: preliminary  
 A|Molecule type: DNA  
 A|Residues: 1-357 <STE2>  
 A|Cross-references: EMBL:X61355; NID:G60179; PID:CAA43622.1; PID:G60180  
 A|Notes: submitted to the EMBL Data Library, July 1991  
 A|Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR  
 A|Reference number: S70417; MUID:92144209; PMID:1736940  
 C|Superfamily: type E retrovirus env polypeptide

Query Match 62.2%; Score 79; DB 2; Length 357;  
 BL local similarity 60.0%; Pred. No. 0.00067;  
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

DB 93 LIGMCSGKLLCTTAVPNN 112

## RESULT 14

522004  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 41)  
 C|Species: human immunodeficiency virus type 1, HIV-1  
 C|Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 A|Accession: S22004, S70419  
 A|Cross-references: EMBL:X61353; NID:G60189; PID:CAA43618.1; PID:G60189  
 A|Residues: 1-357 <STE2>  
 A|Molecule type: DNA  
 A|Notes: submitted to the EMBL Data Library, July 1991  
 A|Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR  
 A|Reference number: S21990

A|Accession: S22004  
 A|Molecule type: DNA  
 A|Residues: 1-357 <STE2>  
 A|Cross-references: EMBL:X61353; NID:G60189; PID:CAA43618.1; PID:G60189  
 A|Residues: 1-357 <STE2>  
 A|Molecule type: DNA  
 A|Notes: submitted to the EMBL Data Library, July 1991  
 A|Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR  
 A|Reference number: S70417; MUID:92144209; PMID:1736940  
 A|Accession: S70419  
 A|Status: preliminary  
 A|Molecule type: DNA  
 A|Residues: 1-357 <STE2>  
 A|Cross-references: EMBL:X61353; NID:G60189  
 A|Notes: submitted to the EMBL Data Library, July 1991  
 A|Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR  
 A|Reference number: S21990  
 C|Superfamily: type E retrovirus env polypeptide

Query Match 62.2%; Score 79; DB 2; Length 357;  
 BL local similarity 60.0%; Pred. No. 0.00067;  
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

DB 93 LIGMCSGKLLCTTAVPNN 112

## RESULT 15

521996  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 271)  
 C|Species: human immunodeficiency virus type 1, HIV-1  
 C|Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 A|Accession: S70422, S21996  
 A|Cross-references: EMBL:X61355; NID:G60179; PID:CAA43622.1; PID:G60180  
 A|Residues: 1-357 <STE2>  
 A|Molecule type: DNA  
 A|Notes: submitted to the EMBL Data Library, July 1991  
 A|Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR  
 A|Reference number: S70417; MUID:92144209; PMID:1736940  
 A|Accession: S70422  
 A|Status: preliminary  
 A|Molecule type: DNA  
 A|Residues: 1-357 <STE2>  
 A|Cross-references: EMBL:X61355; NID:G60179; PID:CAA43622.1; PID:G60180  
 A|Notes: submitted to the EMBL Data Library, July 1991  
 A|Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR  
 A|Reference number: S70417; MUID:92144209; PMID:1736940  
 C|Superfamily: type E retrovirus env polypeptide

Query Match 62.2%; Score 79; DB 2; Length 357;  
 BL local similarity 60.0%; Pred. No. 0.00067;  
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

DB 93 LIGMCSGKLLCTTAVPNN 112

Search completed: May 29, 2003, 10:40:24  
 Job time: 10.8254 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:31:50 ; Search time 5.4127 Seconds

(without alignments)  
168,381 Million cell updates/sec

Title: US-09-147-362a-8

Perfect score: 127

Sequence: 1 LLSWCGRGRVCTSVQNMET 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot\_40.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the best hit being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query	Match Length	DB ID	Description
1	83	65.4	854	1 ENV_HV12Z	P1781 human immun
2	80	63.0	853	1 ENV_HV12Z	P1781 human immun
3	80	63.0	853	1 ENV_HV12Z	P1781 human immun
4	79	62.2	843	1 ENV_HV12Z	P15661 human immun
5	79	62.2	847	1 ENV_HV12Z	P15661 human immun
6	79	62.2	847	1 ENV_HV12Z	P15661 human immun
7	79	62.2	847	1 ENV_HV12Z	P15661 human immun
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9	79	62.2	847	1 ENV_HV12Z	P15661 human immun
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## ALIGNMENTS

RESULT 1	ENV_SIVCZ	STANDARD	PRT	854 AA.
ID	P1781			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-JUL-1993 (Rel. 38, Last annotation update)			
DE	Envelope polypeptide GP16 precursor [Contains: Exterior membrane			
OS	Glycoprotein (GP120); Transmembrane glycoprotein (GP41).			
OR	ENV.			
OC	Chimpanzee immunodeficiency virus (SIV/cpz) (CIV).			
OC	Vitruvian; Retrovirus; Retroviridae; Lentivirus.			
OX	NCBI_TaxID:11723;			
EN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90259077; PubMed=2188136;			
RT	Huet T., Chemtob R., Wehrhans A., Roelants G., Wain-Hobson S.;			
RL	Genetic organization of a chimpanzee lentivirus related to HIV-1."			
CC	-1- SIMILARITY: STRONG, WITH HIV-1 ENV POLYPEPTIDE.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	modification and this statement is not removed as a condition of use by			
CC	or send an email to license@sb.ch.			
DR	EMBL; X52154; CA36407.1; -			
DR	PIR; S09590; VCLJ51.			
DR	HIV; X52154; X52154; ENV GP41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00517; GP120.1.			
DR	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;			
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Best Local Similarity 54.5%; Pred. No. 3.3e-05;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LLSWCGRGRGLVCYSYVNMT 22
582 ILGLMGCSKRGKICITTPVNSS 603

DB

RESULT 2
ENV_HV122 STANDARD; PRT; 853 AA.
AC P12487.1989 (rel. 12; Created)
DT 01-OCT-1989 (rel. 12; Last sequence update)
DT 16-OCT-2001 (rel. 40; Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
OS BNY.
GN Human immunodeficiency virus type 1 (22/CDC-234 isolate) (HIV-1).
NC Nucleus; Retrovirales; Retroviridae; Lentiviridae.
NC [1]_TaxId=11893;
RN [1]_TaxId=11893;
RA Theodore T. Buckler-White A.;
RP SEQUENCE FROM N.A.
RL Submitted (NOV-1988) to the HIV data bank.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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FT CARBOHYD 459 459 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 462 462 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 612 612 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 613 613 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 622 622 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 634 634 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 671 671 N-LINKED (GLCNAC...) (POTENTIAL)
SQ SEQUENCE 853 AA; 97043 MW; 849808CBAFF7008 CRC64;

Query Match 63.0%; Score 80; DB 1; Length 853;
Best Local Similarity 54.5%; Pred. No. 9.6e-05;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LLSWCGRGRGLVCYSYVNMT 22
589 ILGLMGCSKRGKICITTPVNSS 610

DB

RESULT 3
ENV_HV126 STANDARD; PRT; 855 AA.
AC P04560.05 (rel. 05; Created)
DT 13-AUG-1987 (rel. 05; Last sequence update)
DT 13-AUG-1992 (rel. 05; Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
OS BNY.
GN Human immunodeficiency virus type 1 (2a11e 6 isolate) (HIV-1).
NC Nucleus; Retrovirales; Retroviridae; Lentiviridae.
NC [1]_TaxId=11708;
RN [1]_TaxId=11708;
RA MEDLINE FROM N.A.
RP SEQUENCE FROM N.A.
RX SRINIVASAN A., ANAND R., YOK D., RANGANATHAN P., PEORIN P.,
SACHOCHETMAN G., CURRAN J., KALYANESAM V.S., LUTCH P.A.,
SANCHEZ-PESCADOR R.;
RA Molecular characterization of human immunodeficiency virus from
patients with the acquired immunodeficiency syndrome and variable
domains in the envelope gene.
RL Gene 52.71-82(1987).
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[illegible]



MEDLINE=68085613; PubMed=2789516;  
 Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Lucif P.,  
 Dandekar S.;  
 RA "Biological and molecular characterization of human immunodeficiency  
 RT virus (HIV-1BR) from the brain of a patient with progressive  
 dementia.";  
 RL Virology 168:75-89(1998)  
 CC 1- HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.  
 CC -----  
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 CC  
 CC EMBL; M21098; AAA44221.1;  
 DR PIR; A31667; VCLJBR.  
 DR HIV; M21098; EVNSBVA.  
 DR Interpro: IPR000328; Env GP41.  
 DR PIR; M21098; GP41.1.  
 DR Pfam; P000516; GP120.1.  
 DR Pfam; P000517; GP41.1.  
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM  
 FT CHAIN 1 30  
 FT SIGNAL 31 507  
 FT DISULFID 54 832  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 155  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 296 330  
 FT DISULFID 383 412  
 FT DISULFID 49 49  
 FT CARBOHYD 88 88  
 FT CARBOHYD 135 135  
 FT CARBOHYD 138 138  
 FT CARBOHYD 154 154  
 FT CARBOHYD 159 159  
 FT CARBOHYD 234 234  
 FT CARBOHYD 241 241  
 FT CARBOHYD 262 262  
 FT CARBOHYD 276 276  
 FT CARBOHYD 289 289  
 FT CARBOHYD 295 295  
 FT CARBOHYD 303 303  
 FT CARBOHYD 311 311  
 FT CARBOHYD 354 354  
 FT CARBOHYD 360 360  
 FT CARBOHYD 384 384  
 FT CARBOHYD 390 390  
 FT CARBOHYD 396 396  
 FT CARBOHYD 400 400  
 FT CARBOHYD 440 440  
 FT CARBOHYD 456 456  
 FT CARBOHYD 607 607  
 FT CARBOHYD 612 612  
 FT CARBOHYD 621 621  
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 FT CARBOHYD 670 670  
 FT CARBOHYD 717 717  
 FT CARBOHYD 852 852  
 SQ SEQUENCE 852 AA; 97203 MW; 2B866450DE315F CR64;  
 Query Match 63.2%; Score 79; DB 1; Length 852;  
 Best Local Similarity 60.0%; Pred. No. 0.00014;  
 Match 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

RESULT 8  
 ID ENV HTS3 STANDARD; PRF; 852 AA.  
 AC P35649;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 16-OCT-2001 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Envelope polypeptide GP120 precursor (contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)).  
 OS Human immunodeficiency virus type 1 (SP3 isolate) (HIV-1).  
 OC Viruses; Retroviridae; Lentivirinae.  
 NCBI\_TaxID:11590;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90317906; PubMed=270688  
 RX Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Lucif P.,  
 RT "Human immunodeficiency virus type 1 cellular host range,  
 RT replication, and cytopathicity are linked to the envelope region of  
 RT the viral genome.";  
 RL J. Virol. 64:4016-4020(1990).  
 CC -----  
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 CC or send an email to [license@ebd.ch](mailto:license@ebd.ch)).  
 CC  
 CC EMBL; M21098; AAA44221.1;  
 DR PIR; A31667; VCLJBR.  
 DR HIV; M21098; EVNSBVA.  
 DR Interpro: IPR000328; Env GP41.  
 DR PIR; M21098; GP41.1.  
 DR Pfam; P000516; GP120.1.  
 DR Pfam; P000517; GP41.1.  
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM  
 FT CHAIN 1 30  
 FT SIGNAL 31 507  
 FT DISULFID 54 832  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 155  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 296 330  
 FT DISULFID 383 412  
 FT DISULFID 49 49  
 FT CARBOHYD 88 88  
 FT CARBOHYD 135 135  
 FT CARBOHYD 138 138  
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 FT CARBOHYD 159 159  
 FT CARBOHYD 234 234  
 FT CARBOHYD 241 241  
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 FT CARBOHYD 717 717  
 FT CARBOHYD 852 852  
 SQ SEQUENCE 852 AA; 97203 MW; 2B866450DE315F CR64;  
 Query Match 63.2%; Score 79; DB 1; Length 852;  
 Best Local Similarity 60.0%; Pred. No. 0.00014;  
 Match 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;



DR HIV: A03976; VCLJAZ2.  
 DR HIV: M02007; ENVSS82.  
 DR InterPro: IPR000328; Env GP41.  
 DR InterPro: IPR000771; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Transmembrane;  
 K1 SIGNAL  
 FT CHAIN 1 29  
 FT CHAIN 30 509  
 FT CHAIN 510 855  
 FT DISULFID 53 73  
 FT DISULFID 118 208  
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 FT DISULFID 129 250  
 FT DISULFID 231 242  
 FT DISULFID 299 333  
 FT DISULFID 380 442  
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 FT CARBOHYD 87 87  
 FT CARBOHYD 140 140  
 FT CARBOHYD 154 154  
 FT CARBOHYD 158 158  
 FT CARBOHYD 184 184  
 FT CARBOHYD 190 190  
 FT CARBOHYD 200 200  
 FT CARBOHYD 223 223  
 FT CARBOHYD 223 223  
 FT CARBOHYD 255 255  
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 FT CARBOHYD 292 292  
 FT CARBOHYD 298 298  
 FT CARBOHYD 304 304  
 FT CARBOHYD 321 321  
 FT CARBOHYD 321 321  
 FT CARBOHYD 358 358  
 FT CARBOHYD 364 364  
 FT CARBOHYD 388 388  
 FT CARBOHYD 394 394  
 FT CARBOHYD 400 400  
 FT CARBOHYD 408 408  
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 SEQUENCE

Query Match 62.2%; Score 79; DB 1; Length 855;  
 Best Local Similarity 60.0%; Pred. No. 0.00014;  
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

ENV\_HVLOT STANDARD; PRT; 855 AA.  
 AD P0868  
 DT 01-FEB-1991 (Reel. 17, Created)  
 DT 01-FEB-1991 (Reel. 17, Last annotation update)  
 DT 15-JUL-1999 (Reel. 38, Last annotation update)  
 DR Envelope glycoprotein GP120 precursor [Contains: Exterior membrane  
 DR Glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 DR HIV.  
 DR Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).

CC VIRUSES; Retroid viruses; Retroviridae; Lentivirus.  
 RX MEDLINE:90148544; PubMed:2859749;  
 RA Huei T.; Daza M.C.; Brun-Vezinet F.; Roelants G.E.; Main-Hobson S.;  
 RT A highly defective HIV-1 strain isolated from a healthy Gabonese  
 RT individual presenting an atypical Western blot.  
 RL AIDS (Oct 1989).  
 CC MEDLINE:90148544; PubMed:2859749;  
 CC - AIDS (Oct 1989).  
 CC HEALTHY GABONESE INDIVIDUAL  
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 CC EMBL; M26727; AAA83397.1; -  
 DR HIV: M26727; ENVSV1.  
 DR InterPro: IPR000328; Env GP41.  
 DR InterPro: IPR000771; GP120.  
 DR Pfam: PF00517; GP41; 1.  
 DR Pfam: PF00516; GP120; 1.  
 DR AIDS; Coat protein; Glycoprotein; Transmembrane;  
 KW SIGNAL  
 FT CHAIN 1 29  
 FT CHAIN 30 509  
 FT CHAIN 510 855  
 FT DISULFID 53 73  
 FT DISULFID 118 210  
 FT DISULFID 125 201  
 FT DISULFID 130 162  
 FT DISULFID 223 252  
 FT DISULFID 233 244  
 FT DISULFID 291 321  
 FT DISULFID 301 435  
 FT DISULFID 388 415  
 FT CARBOHYD 87 87  
 FT CARBOHYD 134 134  
 FT CARBOHYD 142 142  
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 FT CARBOHYD 151 151  
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 FT CARBOHYD 267 267  
 FT CARBOHYD 281 281  
 FT CARBOHYD 304 304  
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 FT CARBOHYD 336 336  
 FT CARBOHYD 359 359  
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 FT CARBOHYD 853 AA; 97476 MW; G5924607AD822A C64;  
 SEQUENCE

Query Match 62.2%; Score 79; DB 1; Length 855;  
 Best Local Similarity 60.0%; Pred. No. 0.00014;  
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

ENV\_HVLOT STANDARD; PRT; 855 AA.  
 AD P0868  
 DT 01-FEB-1991 (Reel. 17, Created)  
 DT 01-FEB-1991 (Reel. 17, Last annotation update)  
 DT 15-JUL-1999 (Reel. 38, Last annotation update)  
 DR Envelope glycoprotein GP120 precursor [Contains: Exterior membrane  
 DR Glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 DR HIV.  
 DR Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).





[illegible]

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Query Match 63 28; Score 79; DB 1; Length 85;
Best Local Similarity 60 08; Pred. No. 0 00014;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

      1 TTSKNCAGGATCYTSCN 20
      |||||::|::|:|
Db    592 LTGKMGSGALCTTAFFN 611

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Job time : 5.4127 secs

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AC 09DCL9.
DT 01-MAR-2001 (TREMBlrel. 15, Created)
DT 01-MAR-2001 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=SF-W1321;
RC MEDLINE=2058464; PubMed=1153079;
RA O'Callaghan, M., Munoz, L., Bernal, A., Rodriguez A., Zorratino A.,
RT "Molecular characterization of Non-B HIV type 1 Subtypes from Africa
RL AIDS Res. Hum. Retroviruses 16:1967-1971(2000).
EMBL/AZ55929; AAC36894.1;
InterPro: IPR000328; Env_Gp41.
Pfam: PF00517; Gp41; 1.
KW Transmembrane.
FT NON-TER
SQ SEQUENCE 135 AA; 16285 MW; D349BEF7318B36 CRC64;

Query Match 89.8%; Score 114; DB 15; Length 135;
Best Local Similarity 81.8%; Pred. No. 3e-10;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSMCGCRGLVCTSYVQNMET 22
Db 48 LLSMCGCRGLVCTSYVQNMET 69

RESULT 3
091866 PRELIMINARY; PRT; 209 AA.
ID Q91866
AC Q91866
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Env polypeptide, gp41 (fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RC STRAIN=BCF101;
RA Kohn, S., Kohn, D., Darnold, F., Souquiere, S., Mucicler, P.,
RT "Phylogenetic analysis and sub-typing of 47 HIV-1-".
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
EMBL/AJ238862; CAB9300.1;
InterPro: IPR000328; Env_Gp41.
Pfam: PF00517; Gp41; 1.
KW Transmembrane.
FT NON-TER
SQ SEQUENCE 209 AA; 24116 MW; 91AC0B28FE7A893 CRC64;

Query Match 89.0%; Score 113; DB 15; Length 209;
Best Local Similarity 81.8%; Pred. No. 6.7e-10;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSMCGCRGLVCTSYVQNMET 22
Db 56 LLSMCGCRGLVCTSYVQNMET 77

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ID 091866 PRELIMINARY; PRT; 219 AA.
AC 091866
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Gp41 (fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=BCF14;
RA Roques P., Robertson D., Sandrine S., Christel D., Francoise S.,
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates".
RL EMBL/AJ235404; CAB96252.
InterPro: IPR000328; Env_Gp41.
Pfam: PF00517; Gp41; 1.
KW Transmembrane.
FT NON-TER
SQ SEQUENCE 219 AA; 25353 MW; F65829B01520D91 CRC64;

Query Match 88.2%; Score 112; DB 15; Length 219;
Best Local Similarity 81.8%; Pred. No. 1e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSMCGCRGLVCTSYVQNMET 22
Db 57 LLSMCGCRGLVCTSYVQNMET 78

RESULT 5
040458 PRELIMINARY; PRT; 116 AA.
ID 040458
AC 040458
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Envelope transmembrane glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=GROUP O;
RA Bhollier-Ruche F., Ekasa E., Peeters M., Delaporte E.;
RT "Molecular characterization of envelope transmembrane glycoprotein of
RL 14 new human immunodeficiency virus type 1 group O strains from
RT different African countries".
EMBL/AJ238862; CAB9300.1;
InterPro: IPR000328; Env_Gp41.
Pfam: PF00517; Gp41; 1.
KW Transmembrane.
FT NON-TER
SQ SEQUENCE 116 AA; 13653 MW; 540F5B3B7AD84908 CRC64;

Query Match 86.4%; Score 110; DB 15; Length 116;
Best Local Similarity 77.3%; Pred. No. 1.1e-09;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSMCGCRGLVCTSYVQNMET 22
Db 39 LLSMCGCRGLVCTSYVQNMET 60

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RESULT 4
091866 PRELIMINARY; PRT; 124 AA.
ID Q91866

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AC 091H07;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (fragment).
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RS STRAIN=97CWT98;
RC MEDLINE=20386754; PubMed=10933623;
RA Yang C., Gao F., Fontjuno P.N., Zekeng L., van der Groen G.,
RA Pleniasek D., Schable C., Lal R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O.";
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR InterPro: IP000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KM Transmembrane.
FT NON TER 1 1
FT NON TER 124 124
SQ SEQUENCE 124 AA; 15187 MW; 105D515F114450F8 CRC64;
Query Match 86.6%; Score 110; DB 15; Length 124;
Best Local Similarity 77.3%; Pred. No. 1.2e-09;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
OY 1 LLSWCGKGRGLVCTYSVKNMET 22
DB 33 LLSWCGKGRGLVCTYSVKNMET 54

RESULT 7
O91H07;
AC 091H07;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RS STRAIN=97CWT98;
RC MEDLINE=20386754; PubMed=10933623;
RA Yang C., Gao F., Fontjuno P.N., Zekeng L., van der Groen G.,
RA Pleniasek D., Schable C., Lal R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O.";
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR InterPro: IP000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KM Transmembrane.
FT NON TER 1 1
FT NON TER 126 126
SQ SEQUENCE 126 AA; 15169 MW; 13F010EBCDF0DD CRC64;
Query Match 86.6%; Score 110; DB 15; Length 126;
Best Local Similarity 86.6%; Pred. No. 1.2e-09;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY 1 LLSWCGKGRGLVCTYSVKNMET 22
DB 40 LLSWCGKGRGLVCTYSVKNMET 61

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RESULT 8
O91H09;
AC 091H09;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (fragment).
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RS STRAIN=97CWT98;
RC MEDLINE=20386754; PubMed=10933623;
RA Yang C., Gao F., Fontjuno P.N., Zekeng L., van der Groen G.,
RA Pleniasek D., Schable C., Lal R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O.";
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR InterPro: IP000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KM Transmembrane.
FT NON TER 1 1
FT NON TER 130 130
SQ SEQUENCE 130 AA; 15593 MW; 5385789A36344EA CRC64;
Query Match 86.6%; Score 110; DB 15; Length 130;
Best Local Similarity 77.3%; Pred. No. 1.2e-09;
Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
OY 1 LLSWCGKGRGLVCTYSVKNMET 22
DB 40 LLSWCGKGRGLVCTYSVKNMET 61

RESULT 9
O91B95;
AC 091B95;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GP41 (fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RS STRAIN=YBF51;
RC SEQUENCE FROM N.A.
RA Riquies P., Robertson D., Sandline S., Chistrel D., Francois S.,
RA Phillips M.;
RT "Phylogenetic analysis and sub-typing of 42 HIV-1 group O isolates.";
RL Submitted (JUN-1998) to the EMBL/Genbank/DBS databases.
DR InterPro: IP000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KM Transmembrane.
FT NON TER 1 1
FT NON TER 218 218
SQ SEQUENCE 218 AA; 25243 MW; E7F0E1E20E79PA8 CRC64;
Query Match 86.6%; Score 110; DB 15; Length 218;
Best Local Similarity 77.3%; Pred. No. 2.1e-09;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
OY 1 LLSWCGKGRGLVCTYSVKNMET 22
DB 54 LLSWCGKGRGLVCTYSVKNMET 75

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## RESULT 10

Q91E82 PRELIMINARY; PRT; 230 AA.

AC Q91E82; 2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Gp41 (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxId:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Roqueas P., Robertson D., Sandrine S., Christel D., Francois S.,  
 RA Philippe M.,  
 RA Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
 Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 EMBL:U08-192863.1; Genbank:U08-192863.1; F0000128; InterPro: IPR000128; Enr:  
 InterPro: IPR000128; Enr:  
 Pfam: PF00517; Gp41.1; \_Gp41.  
 DR InterPro: IPR000128; Gp41.1; \_Gp41.  
 DR Transmembrane.  
 KM Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 230 230

SQ SEQUENCE 230 AA; 26705 MW; C1F744F82F51302D CRC64;

Query Match 86.6%; Score 110; DB 15; Length 230;

Best Local Similarity: 77.3%; Pfam No. 2.2e-09; Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLSMCGCRGLVCYTSVQNNET 22  
 DB 55 LLLMGCKGRRLICVTSVANNET 76

## RESULT 11

Q91E32 PRELIMINARY; PRT; 240 AA.

AC Q91E32; 2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE TM, Gp41 (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxId:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Roqueas P., Robertson D., Souquiere S., Diamond F., Mauciere P.,  
 RA Depienne C., Brun-Vezinet F., Dormont D., Simon F.O.,  
 RA Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates."  
 Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 EMBL:U08-192863.1; Genbank:U08-192863.1; F0000128; InterPro: IPR000128; Enr:  
 InterPro: IPR000128; Enr:  
 Pfam: PF00517; Gp41.1; \_Gp41.  
 DR InterPro: IPR000128; Gp41.1; \_Gp41.  
 DR Transmembrane.  
 KM Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 240 240

SQ SEQUENCE 240 AA; 27723 MW; 1E206BD491A4197 CRC64;

Query Match 86.6%; Score 110; DB 15; Length 240;

Best Local Similarity: 77.3%; Pfam No. 2.2e-09; Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLSMCGCRGLVCYTSVQNNET 22  
 DB 60 LLLMGCKGRRLICVTSVANNET 81

## RESULT 12

Q91E85 PRELIMINARY; PRT; 536 AA.

AC Q91E85; 2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Gp41 polypeptide (fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxId:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Roqueas P., Robertson D., Souquiere S., Mauciere P.,  
 RA Depienne C., Brun-Vezinet F., Dormont D., Simon F.O.,  
 RA "HIV-1 group O phylogenetic analysis of C2-gp41 region."  
 Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.  
 EMBL:AJ133062; Genbank:AJ133062.1; F0000128; InterPro: IPR000128; Enr:  
 InterPro: IPR000128; Gp41.1; \_Gp41.  
 DR InterPro: IPR000128; Gp41.1; \_Gp41.  
 DR Transmembrane.  
 KM Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 536 536

SQ SEQUENCE 536 AA; 60419 MW; 0F533A8AF08F552 CRC64;

Query Match 86.6%; Score 110; DB 15; Length 536;

Best Local Similarity: 77.3%; Pfam No. 5.1e-09; Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLSMCGCRGLVCYTSVQNNET 22  
 DB 361 LLLMGCKGRRLICVTSVANNET 382

## RESULT 13

Q91E05 PRELIMINARY; PRT; 538 AA.

AC Q91E05; 2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ENV polypeptide (fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxId:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Roqueas P., Robertson D., Souquiere S., Mauciere P.,  
 RA Depienne C., Brun-Vezinet F., Dormont D., Simon F.O.,  
 RA "HIV-1 group O phylogenetic analysis of C2-gp41 region."  
 Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.  
 EMBL:AJ133062; Genbank:AJ133062.1; F0000128; InterPro: IPR000128; Enr:  
 InterPro: IPR000128; Gp41.1; \_Gp41.  
 DR InterPro: IPR000128; Gp41.1; \_Gp41.  
 DR Transmembrane.  
 KM Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 538 538

SQ SEQUENCE 538 AA; 60777 MW; B1C956A233F8FD CRC64;

Query Match 86.6%; Score 110; DB 15; Length 538;

Best Local Similarity: 77.3%; Pfam No. 5.1e-09; Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLSMCGCRGLVCYTSVQNNET 22  
 DB 361 LLLMGCKGRRLICVTSVANNET 382





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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:30:20, Search time 21.333 Seconds

99.336 Million cell updates/sec

Title: US-09-147-362a-9

Sequence: 1 LHSWGCKRLVCTYS 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter: 45 summaries

Database :  
1: /SID2/gcgdata/geneseq/genescp-emb1/AA1980.DAT.\*  
2: /SID2/gcgdata/geneseq/genescp-emb1/AA1981.DAT.\*  
3: /SID2/gcgdata/geneseq/genescp-emb1/AA1982.DAT.\*  
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18: /SID2/gcgdata/geneseq/genescp-emb1/AA1997.DAT.\*  
19: /SID2/gcgdata/geneseq/genescp-emb1/AA1998.DAT.\*  
20: /SID2/gcgdata/geneseq/genescp-emb1/AA1999.DAT.\*  
21: /SID2/gcgdata/geneseq/genescp-emb1/AA2000.DAT.\*  
22: /SID2/gcgdata/geneseq/genescp-emb1/AA2001.DAT.\*  
23: /SID2/gcgdata/geneseq/genescp-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	100.0	16	19	AA00467
2	91	100.0	22	19	AA00461
3	91	100.0	22	19	AA00462
4	88	96.7	16	19	AA00468
5	88	96.7	22	19	AA00472
6	88	96.7	22	19	AA00477
7	88	96.7	26	19	AA00475
8	88	96.7	33	21	AA012212
9	88	96.7	33	21	AA012231
10	88	96.7	40	17	AA07346

11	88	96.7	40	17	AA07352	Partial sequence o
12	87	95.6	22	19	AA00463	Peptide derived fr
13	87	95.6	22	19	AA00464	Peptide derived fr
14	86	94.5	40	17	AA07345	Partial sequence o
15	85	93.4	32	19	AA00469	Peptide derived fr
16	85	93.4	33	21	AA012226	Partial sequence o
17	85	93.4	40	17	AA07346	Partial sequence o
18	84	92.3	17	19	AA00474	Peptide derived fr
19	82	90.1	22	19	AA00460	Peptide derived fr
20	82	90.1	23	20	AA005623	Partial sequence o
21	82	90.1	23	20	AA005624	Partial sequence o
22	82	90.1	24	20	AA005625	Partial sequence o
23	82	90.1	24	20	AA005626	Partial sequence o
24	82	90.1	32	22	AA005619	Human immunodefici
25	82	90.1	33	21	AA012207	Partial sequence o
26	82	90.1	33	21	AA012210	Partial sequence o
27	82	90.1	33	21	AA012213	Partial sequence o
28	82	90.1	33	21	AA012214	Partial sequence o
29	82	90.1	42	17	AA007150	Partial sequence o
30	82	90.1	42	17	AA007150	Partial sequence o
31	82	90.1	116	20	AA005555	HIV-1 group O isol
32	82	90.1	117	20	AA005548	HIV-1 group O isol
33	82	90.1	129	19	AA069318	Anti-HIV-1 group O
34	82	90.1	129	19	AA077258	Anti-HIV-1 group O
35	82	90.1	150	19	AA069319	Anti-HIV-1 group O
36	82	90.1	150	19	AA069320	Anti-HIV-1 group O
37	82	90.1	200	11	AA072558	Enkephalin AN70 r
38	82	90.1	200	23	AA068379	Enkephalin AN70 r
39	82	90.1	715	20	AA005615	HIV-1 group O isol
40	81	89.0	715	20	AA005615	HIV-1 group O isol
41	81	89.0	23	20	AA005619	HIV-1 group O extra
42	81	89.0	23	20	AA005622	HIV-1 group O extra
43	81	89.0	23	21	AA012254	HIV-1 gp41 immunod
44	81	89.0	23	21	AA012255	HIV-1 gp41 immunod
45	81	89.0	23	21	AA012256	HIV-1 gp41 immunod

## ALIGNMENTS

RESULT 1

ID AA00467 standard; peptide; 16 AA.

AC AA00467;

XX 28-JAN-1999 (first entry)

DT Peptide derived from a conserved sequence of group O human HIV.

KW Group O human immunodeficiency virus; HIV; detection; infection.

OS Synthetic.

CS Immune deficiency virus.

XX W09845321-A1.

PD 15-OCT-1998.

XX 06-APR-1998; 98MO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

XX 09-APR-1997; 97FR-0004356.

PA (SNP1) PASTEIR SANOPI DIAGNOSTICS SA.

XX Cheneboux DMB, Delagrange JFH, Godelle SIX, Rieunier FY.

DR WPI; 1998-SB1350/49.

XX New synthetic peptide(s) - useful for, e.g. detecting infection by

PT human immunodeficiency virus of group O

PS Claim 6; Page 43; 55pp; French.  
 CC AA080459-74 represent synthetic peptides (either linear or cyclized by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 SO Sequence 16 AA;  
 Query Match 100.0%; Score 91; DB 19; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LLSWCKGRIVCYTS 16  
 Db 1 LLSWCKGRIVCYTS 16  
 ID AA080461 standard; peptide; 22 AA.  
 AC AA080461;  
 XX AA080461;  
 XX 28-JUN-1999 (first entry)  
 DT Peptide derived from a conserved sequence of group O human HIV.  
 DE Group O human immune deficiency virus; HIV; detection; infection.  
 XX Group O human immune deficiency virus; HIV; detection; infection.  
 XX Synthetic.  
 OS Immune deficiency virus.  
 CC Immune deficiency virus.  
 XX WO9845323-A1.  
 XX 15-OCT-1998.  
 XX 06-APR-1998; 98WO-FR00691.  
 XX 24-FEB-1998; 98FR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.  
 XX Chenebaux DMB, Delagneau JFH, Gadelle SJX, Rieunier FY;  
 PI WPI: 1998-583190/49.  
 PF New synthetic peptide(s) - useful for, e.g. detecting infection by  
 PF human immune deficiency virus of group O  
 Claim 6; Page 42; 55pp; French.  
 CC AA080459-74 represent synthetic peptides (either linear or cyclized by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 SO Sequence 22 AA;  
 Query Match 100.0%; Score 91; DB 19; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LLSWCKGRIVCYTS 16  
 Db 1 LLSWCKGRIVCYTS 16

RESULT 3  
 ID AA080462  
 XX AA080462 standard; peptide; 22 AA.  
 AC AA080462;  
 XX 28-JUN-1999 (first entry)  
 DT Peptide derived from a conserved sequence of group O human HIV.  
 DE Group O human immune deficiency virus; HIV; detection; infection.  
 XX Group O human immune deficiency virus; HIV; detection; infection.  
 XX Synthetic.  
 OS Immune deficiency virus.  
 CC Immune deficiency virus.  
 XX WO9845323-A1.  
 XX 15-OCT-1998.  
 XX 06-APR-1998; 98WO-FR00691.  
 XX 24-FEB-1998; 98FR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 XX (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.  
 XX Chenebaux DMB, Delagneau JFH, Gadelle SJX, Rieunier FY;  
 PI WPI: 1998-583190/49.  
 PF New synthetic peptide(s) - useful for, e.g. detecting infection by  
 PF human immune deficiency virus of group O  
 Claim 6; Page 42; 55pp; French.  
 CC AA080459-74 represent synthetic peptides (either linear or cyclized by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 SO Sequence 22 AA;  
 Query Match 100.0%; Score 91; DB 19; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LLSWCKGRIVCYTS 16  
 Db 1 LLSWCKGRIVCYTS 16  
 ID AA080468 standard; peptide; 16 AA.  
 AC AA080468;  
 XX 28-JUN-1999 (first entry)  
 DT Peptide derived from a conserved sequence of group O human HIV.  
 DE Group O human immune deficiency virus; HIV; detection; infection.  
 XX Group O human immune deficiency virus; HIV; detection; infection.  
 XX Synthetic.  
 OS Immune deficiency virus.  
 CC Immune deficiency virus.  
 XX WO9845323-A1.  
 XX 15-OCT-1998.  
 XX 06-APR-1998; 98WO-FR00691.

24-FEB-1996; 98PR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 XX (SNFI ) PASTEUR SANOPI DIAGNOSTICS SA.  
 XX  
 XX  
 PI Chenebaux DMB, Delagrange JFH, Gabelle SXJ, Rieunier FY;  
 XX WPI; 1996-583190/49.  
 DR  
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
 PT human immune deficiency virus of group O  
 PT  
 PI Claim 6; Page 43; 55pp; French.  
 CC  
 CC AAM80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 Db Sequence 16 AA:  
 96;74; Score 88; DB 19; Length 16;  
 Query Match  
 Best Local Similarity 93.84; Pred. No. 2;7e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0.  
 1 ILSGCGCGGLGCTGNS 16  
 |||:|||||||  
 1 LINSWCGKRLVCTYS 16  
 RESULT 5  
 AAM80472  
 ID AAM80472 standard; peptide; 22 AA.  
 XX  
 XX AAM80472;  
 XX  
 DT 28-JAN-1999 (first entry)  
 DE Peptide derived from a conserved sequence of group O human HIV.  
 XX Group O human immune deficiency virus; HIV; detection; infection.  
 XX  
 XX Synthetic.  
 OS Immune deficiency virus.  
 MO9845323-A1.  
 PD 15-OCT-1998.  
 PD 06-APR-1998; 98MO-FR00661.  
 PR 24-FEB-1998; 98PR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 PA (SNFI ) PASTEUR SANOPI DIAGNOSTICS SA.  
 PA  
 PI Chenebaux DMB, Delagrange JFH, Gabelle SXJ, Rieunier FY;  
 XX WPI; 1996-583190/49.  
 PT  
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
 PT human immune deficiency virus of group O  
 PT  
 PI Claim 6; Page 44; 55pp; French.  
 CC  
 CC AAM80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O

CC	human immune deficiency virus (HIV).
XX	
SQ	Sequence 22 AA.
QY	96.7% Score 88; DB 19; Length 22;
Query Match	Best Local Similarity 93.8%; Pred. No. 3.7e-06;
Matches	15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB	1 LLSMCKGRGLVCTYS 16     6 LLSMCKGRGLVCTYS 21
RESULT 5	
AAW80466	ID AAW80466 standard; peptide: 22 AA.
AC	AAW80466;
AD	28-JAN-1999 (first entry)
DE	Peptide derived from a conserved sequence of group O human HIV.
DX	
KW	Group O human immune deficiency virus; HIV; detection; infection.
OS	Synthetic.
QS	Immune deficiency virus.
PM	M09645323-AI.
PD	15-OCT-1998.
PF	06-APR-1998; 98MO-FR00691.
PR	24-FEB-1998; 98EP-0002212.
PK	03-APR-1997; 97FR-0004356.
PA	(SMFI ) PASTEUR SANOPI DIAGNOSTICS SA.
FJ	
FX	Cheneboux DMB, Delageau JFH, Gadelle SJX, Rieunier FY;
WP	1998-583190/49.
XX	New synthetic peptide(e) - useful for e.g. detecting infection by human immune deficiency virus of group O
PS	Claim 6; Page 43; 55pp; French.
XX	
AM80459-74	represent synthetic peptides (either linear or cyclised by Cys-Cys disulphide bonds). The peptides represent variable sequences connected around short highly conserved sequences present in isolates of group O human immune deficiency virus. They are designed to detect human immune deficiency virus (HIV).
SQ	Sequence 22 AA;
Query Match	96.7% Score 88; DB 19; Length 22;
Best Local Similarity	93.8%; Pred. No. 3.7e-06;
Matches	15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY	1 LLSMCKGRGLVCTYS 16     1 LLSMCKGRGLVCTYS 16
DB	
RESULT 7	
AAW80473	ID AAW80473 standard; peptide: 28 AA.
AC	AAW80473;
AD	28-JAN-1999 (first entry)
DT	

XX Peptide derived from a conserved sequence of group O human HIV.  
 XX Group O human immune deficiency virus; HIV; detection; infection.  
 XX Synthetic.  
 XX Immune deficiency virus.  
 XX MO9845333-A1.  
 XX 15-OCT-1998.  
 PD 06-APR-1998: 98MO-FR006931.  
 PR 24-FEB-1998: 98FR-0002313.  
 PR 09-APR-1997: 97FR-0004356.  
 XX (SNFI) PASTERE SANOFI DIAGNOSTICS SA.  
 PA Chenboux DMG, Delagneau JFH, Gabelle SDX, Rieunier FY;  
 XX WPI: 1998-583190/49.  
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
 PT human immune deficiency virus of group O  
 XX Claim 6, Page 44: 55pp; French.  
 CC AA080459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds) of the immunodominant variable sequences  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 XX Sequence 28 AA:  
 SO Query Match 96.7%; Score 88; DB 19; Length 28;  
 Best Local Similarity 93.8%; Pred. No. 4.6e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LLSMCGCKGRIVCYTS 16  
 Db 14 LLSMCGCKGRIVCYTS 27  
 XX  
 XX RESULT 8  
 XX AAB12212  
 AC AAB12212 standard; peptide; 33 AA.  
 AC AAB12212;  
 DT 10-NOV-2000 (first entry)  
 DB Partial sequence of HIV-1 strain BCF13 gp41 immunodominant region.  
 XX HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;  
 XX acquired immunodeficiency syndrome; group O HIV; gp41; BCF13.  
 OS Human immunodeficiency virus type 1.  
 XX BP1013766-A2.  
 XX 28-JUN-2000.  
 XX 29-NOV-1999: 99SEP-0109491.  
 PR 30-NOV-1998: 98US-0110292.  
 PR 08-FEB-1999: 99US-0119138.  
 PR 04-NOV-1999: 99US-0433428.  
 XX (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.  
 XX

PI De Lays R, Zheng J;  
 XX WPI: 2000-402205/35.  
 PT New antigenic peptides and peptide functional derivatives, useful for  
 PT detection of antibodies produced in response to human immunodeficiency  
 PT virus group O antibodies -  
 XX Example 1; Fig 1; 52pp; English.  
 CC The present sequence is a partial gp41 protein of human immunodeficiency  
 CC virus type 1 (HIV-1) strain BCF13. HIV is the principle aetiological  
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV  
 CC envelope protein, and may be used as an antigen for the detection of  
 CC HIV group O (outlier). The present sequence is the immunodominant region  
 CC of gp41. This sequence was used in a sequence homology alignment.  
 CC 147 (AAB12254).  
 XX Sequence 33 AA:  
 SO Query Match 96.7%; Score 88; DB 21; Length 33;  
 Best Local Similarity 93.8%; Pred. No. 5.4e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LLSMCGCKGRIVCYTS 16  
 Db 14 LLSMCGCKGRIVCYTS 29  
 XX  
 XX RESULT 9  
 XX AAB12231  
 ID AAB12231 standard; peptide; 33 AA.  
 AC AAB12231;  
 AC AAB12231;  
 DT 10-NOV-2000 (first entry)  
 DB Partial sequence of HIV-1 strain MAN gp41 immunodominant region.  
 XX HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;  
 XX acquired immunodeficiency syndrome; group O HIV; gp41; MAN.  
 OS Human immunodeficiency virus type 1.  
 XX BP1013766-A2.  
 XX 28-JUN-2000.  
 XX 29-NOV-1999: 99SEP-0109491.  
 PR 30-NOV-1998: 98US-0110292.  
 PR 08-FEB-1999: 99US-0119138.  
 PR 04-NOV-1999: 99US-0433428.  
 XX (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.  
 XX De Lays R, Zheng J;  
 XX WPI: 2000-402205/35.  
 PT New antigenic peptides and peptide functional derivatives, useful for  
 PT detection of antibodies produced in response to human immunodeficiency  
 PT virus group O antibodies -  
 XX Example 1; Fig 1; 52pp; English.  
 CC The present sequence is a partial gp41 protein of human immunodeficiency  
 CC virus type 1 (HIV-1) strain MAN. HIV is the principle aetiological  
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV  
 CC envelope protein, and may be used as an antigen for the detection of  
 CC antibodies produced in response to HIV infection. MAN is a member of

CC HIV group O (outlier). The present sequence is the immunodominant region  
 CC of gp41. This sequence was used to derive a consensus sequence peptide: peptide  
 CC which in turn was used to derive a consensus sequence peptide: peptide  
 CC 147 (AAH12254).

XX Sequence 33 AA;

Query Match 96.7%; Score 88; DB 21; Length 33;  
 Similarity 93.8%; Pred. No. 5-4e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Dy 1 LLSMGCKGRIVCYTS 16  
 |||:|||||  
 14 LLSMGCKGRIVCYTS 29

RESULT 10  
 ID AAM07346 standard; peptide; 40 AA.

AAW07346;

03-JUN-1997 (first entry)

Partial sequence of gp41 from HIV-1 gp. O strain BCF07 (MAN).

Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;  
 C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;  
 primer; hybridisation; amplification; PCR; polymerase chain reaction;  
 immunogen; antibody.

Human immunodeficiency virus type 1.

MO627013-A1.

06-SEP-1996.

26-FEB-1996; 96MO-FR00294.

27-FEB-1995; 95FR-0002236.

(ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

Chaix-Baudier ML, Lousseer-Ajaka I, Ly T, Saragosti S, Simon F;

WP1; 1996-412779/41.

N-FSDB; AAH14922.

Claim 12; Page 34; 71pp; French.

Human immunodeficiency virus type 1 (HIV-1) strains are currently  
 divided into 2 major groups based on the nucleotide sequences of the  
 C2V3-env gene (env): group M containing sub-groups A-G and group O  
 containing the strains AN70 and WY0180. The invention relates to the  
 discovery of several new strains of HIV-1 which can be placed in group O,  
 based on the partial sequences of the C2V3-env, gp41 and gag genes (see  
 AA14907-39 and AAM07329-64). The novel strains have been deposited as  
 retroviruses CMC1-1544 (BCF02 (BS)), 1543 (BCF01 (PAN)), 1546 (BCF07  
 (MAN)), 1547 (BCF08 (HKO)) and 1545 (BCF03 (BOC)). The sequence  
 of the gp41 protein encoded by the gag gene and the nucleotide sequence of  
 the gp41 protein encoded by the gag gene can be used as primers for  
 amplification, also for screening and typing of such strains. Peptides  
 encoded by the nucleotide acids can be used as immunogens to raise Ab for  
 detecting gp. O HIV-1.

Sequence 40 AA;

Query Match 96.7%; Score 88; DB 17; Length 40;  
 Similarity 93.8%; Pred. No. 5-5e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Dy 1 LLSMGCKGRIVCYTS 16  
 |||:|||||  
 19 LLSMGCKGRIVCYTS 34

RESULT 11  
 ID AAM07352 standard; peptide; 40 AA.

AAW07352;

03-JUN-1997 (first entry)

Partial sequence of gp41 from HIV-1 gp. O strain BCF1.

Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;  
 C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;  
 primer; hybridisation; amplification; PCR; polymerase chain reaction;  
 immunogen; antibody.

Human immunodeficiency virus type 1.

MO627013-A1.

06-SEP-1996.

26-FEB-1996; 96MO-FR00294.

27-FEB-1995; 95FR-0002236.

(ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

Chaix-Baudier ML, Lousseer-Ajaka I, Ly T, Saragosti S, Simon F;

WP1; 1996-412779/41.

N-FSDB; AAH14922.

Claim 12; Page 46; 71pp; French.

Human immunodeficiency virus type 1 (HIV-1) strains are currently  
 divided into 2 major groups based on the nucleotide sequences of the  
 C2V3-env gene (env): group M containing sub-groups A-G and group O  
 containing the strains AN70 and WY0180. The invention relates to the  
 discovery of several new strains of HIV-1 which can be placed in group O,  
 based on the partial sequences of the C2V3-env, gp41 and gag genes (see  
 AA14907-39 and AAM07329-64). The novel strains have been deposited as  
 retroviruses CMC1-1544 (BCF02 (BS)), 1543 (BCF01 (PAN)), 1546 (BCF07  
 (MAN)), 1547 (BCF08 (HKO)) and 1545 (BCF03 (BOC)). The sequence  
 of the gp41 protein encoded by the gag gene and the nucleotide sequence of  
 the gp41 protein encoded by the gag gene can be used as primers for  
 amplification, also for screening and typing of such strains. Peptides  
 encoded by the nucleotide acids can be used as immunogens to raise Ab for  
 detecting gp. O HIV-1.

Sequence 40 AA;

Query Match 96.7%; Score 88; DB 17; Length 40;  
 Similarity 93.8%; Pred. No. 5-5e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Dy 1 LLSMGCKGRIVCYTS 16  
 |||:|||||  
 19 LLSMGCKGRIVCYTS 34

RESULT 12  
AA80463  
ID AA80463 standard; peptide; 22 AA.  
XX  
XX  
XX AA80463;  
XX  
XX  
XX 28-JAN-1999 (first entry)  
XX  
XX  
XX Peptide derived from a conserved sequence of group O human HIV.  
XX  
XX Group O human immune deficiency virus; HIV; detection; infection.  
XX  
XX Synthetic  
XX Immune deficiency virus.  
XX  
XX W09845323-A1.  
XX  
XX 15-OCT-1998.  
XX  
XX 06-APR-1998; 98WO-FR00691.  
XX  
XX 24-FEB-1998; 98FR-0002212.  
XX 09-APR-1997; 97FR-0004356.  
XX  
XX (SNF1) PASTEUR SMOFT DIAGNOSTICS SA.  
XX  
XX  
XX Cheneboux DMB, Delagneau JPH, Godelle SOX, Kleunier FY;  
XX WPI; 1998-561390/49.  
XX  
XX  
XX New synthetic peptide(s) - useful for, e.g. detecting infection by  
XX human immune deficiency virus of group O  
XX  
XX Claim 6; Page 42; 55pp; French.  
XX  
XX AA80459-74 represent synthetic peptides (either linear or cyclized by  
XX Cys-Cys disulphide bonds). The peptides represent variable sequences  
XX connected around short highly conserved sequences present in isolates  
XX of group O human immune deficiency virus (HIV). The peptides are  
XX useful as immunological reagents for detecting infection by group O  
XX human immune deficiency virus (HIV).  
XX  
XX Sequence 22 AA;  
XX  
XX  
XX Query Match 95.6%; Score 87; DB 19; Length 22;  
XX Best Local Similarity 93.8%; Pred. No. 5.1e-06;  
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 LLSWGCKGRVCTTS 16  
XX 1 LLSWGCKGRVCTTS 16  
XX 1 LLSWGCKGRVCTTS 16  
XX 1 LLSWGCKGRVCTTS 16  
XX  
XX RESULT 13  
XX AA812236  
XX ID AA812236 standard; peptide; 33 AA.  
XX  
XX AA812236;  
XX  
XX 10-NOV-2000 (first entry)  
XX  
XX  
XX Partial sequence of HIV-1 strain ESS gp41 immunodominant region.  
XX  
XX HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;  
XX acquired immunodeficiency syndrome; group O HIV; gp41; ESS.  
XX  
XX Human immunodeficiency virus type 1.  
XX  
XX EF103766-A2.  
XX  
XX 28-JUN-2000.  
XX  
XX

XX 29-NOV-1999; 99EP-030949L.  
XX  
XX 30-NOV-1998; 98US-0110292.  
XX 08-FEB-1999; 99US-0119138.  
XX 04-NOV-1999; 99US-0433428.  
XX  
XX (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.  
XX  
XX  
XX De Leye R, Zheng J;  
XX  
XX WPI; 2000-402205/35.  
XX  
XX  
XX New antigenic peptides and peptide functional derivatives, useful for  
XX detection of antibodies produced in response to human immunodeficiency  
XX virus group O antibodies.  
XX  
XX Example 1; Fig 1; 52pp; English.  
XX  
XX The present sequence is a partial gp41 protein of Human Immunodeficiency  
XX virus type 1 (HIV-1) strain ESS. HIV is the principle aetiological  
XX agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV  
XX surface glycoprotein. It is composed of two subunits, gp120 and gp41.  
XX antibodies produced in response to HIV infection ESS is a member of  
XX HIV group O (outlier). The present sequence is the immunodominant region  
XX of gp41. This sequence was used in a sequence homology alignment  
XX which in turn was used to derive a consensus sequence peptide: peptide  
XX 147 (AA812254).  
XX  
XX  
XX Sequence 33 AA;  
XX  
XX  
XX Query Match 94.5%; Score 86; DB 21; Length 33;  
XX Best Local Similarity 87.5%; Pred. No. 1.1e-05;  
XX Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 LLSWGCKGRVCTTS 16  
XX 1 LLSWGCKGRVCTTS 16  
XX 1 LLSWGCKGRVCTTS 16  
XX 1 LLSWGCKGRVCTTS 16  
XX  
XX RESULT 14  
XX AA807343  
XX ID AA807343 standard; peptide; 40 AA.  
XX  
XX AA807343;  
XX  
XX 03-JUN-1997 (first entry)  
XX  
XX  
XX Partial sequence of gp41 from HIV-1 gp. O strain BCF02 (ESS).  
XX  
XX Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;  
XX acquired immunodeficiency syndrome; AIDS; gp41; hypervariable loop;  
XX primer hybridization; amplification; PCR; polymerase chain reaction;  
XX immunogen; antibody.  
XX  
XX Human immunodeficiency virus type 1.  
XX  
XX W0667013-A1.  
XX  
XX 06-SEP-1996.  
XX  
XX 26-FEB-1996; 96WO-FR00294.  
XX  
XX 27-FEB-1995; 95FR-0002236.  
XX  
XX (ASST-) ASSISTANCE PUBLIQUE HOPITALUX PARIS  
XX (INRA) INSERM INST NAT SANTE & RECH MEDICALE.  
XX  
XX Chaix-Baudier M, Louselet-Ajaja I, Ly T, Saragosti S, Simon F;  
XX WPI; 1996-412779/41.  
XX N-PSDB; AAT44918.  
XX  
XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and



PT antibodies - useful for diagnosis, screening and typing, or as  
 PT immunogens  
 XX  
 PS Claim 12, Page 33, 71pp, French.  
 CC Human immunodeficiency virus type 1 (HIV-1) strains are currently  
 CC divided into 2 major groups based on the nucleotide sequences of the  
 CC envelope gene (env): group M containing sub-groups A-G, and group O.  
 CC In contrast, the strain AM80459 and 1547, the invention relates to the  
 CC group O strains of HIV-1. The novel strains have been deposited as  
 CC based on the partial sequences of the *gag* and *gag* genes (see  
 CC AR44907-39 and AM80732-64). The novel strains have been deposited as  
 CC (NAM), 1547 (BCP08 (RKO)), and 1545 (BCP03 (POC)). The sequence  
 CC presented here is from the strain BCP02 (ESB) and corresponds to a  
 CC fragment of the *gag* protein encoded by the *env* gene. The nucleic acids  
 CC can be used to detect gp. O HIV-1 strains by hybridization or (as  
 CC such as the BCP02 (ESB) and BCP03 (POC) strains) by PCR. The  
 CC strains. Peptides encoded by the nucleic acids can be used as immunogens  
 CC to raise Ab for detecting gp. O HIV-1.

Sequence 40 AA:

Query Match 94.5%; Score 86; DB 17; Length 40;  
 Best Local Similarity 87.5%; Pred. No. 1.3e-05;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWCKGKRIVCYTS 16  
 ||:|||||:  
 DB 19 LLSWCKGKRIVCYTS 34

RESULT 15

AA80459  
 ID AM80469 standard; peptide: 32 AA.

AC AM80469;

XX 28-JAN-1999 (first entry)

XX Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

OS Immune deficiency virus.

XX MO9845323-41.

15-OCT-1998.

PF 06-APR-1998; 98MO-FR00691.

XX 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

XX (SNFI ) PASTEUR SANOPI DIAGNOSTICS SA.

XX Chenebaux DMB, Delagneau JFH, Gabelle SIX, Rieunier FY;

DR WPI; 1998-583190/49.

XX New synthetic peptide(s) - useful for, e.g. detecting infection by

XX human immune deficiency virus of group O

XX Claim 6; Page 44, 55pp; French.

CC AM80459-74 represent synthetic peptides (either linear or cyclised by

CC Cys-Cys disulphide bonds). The peptides represent variable sequences

CC connected around short highly conserved sequences present in isolates

CC of group O human immune deficiency virus (HIV). The peptides are

CC useful as immunological reagents for detecting infection by group O

CC human immune deficiency virus (HIV).

XX Sequence 32 AA:

Query Match 93.4%; Score 85; DB 19; Length 32;  
 Best Local Similarity 87.5%; Pred. No. 1.4e-05;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSWCKGKRIVCYTS 16  
 ||:|||||:  
 DB 11 LLSWCKGKRIVCYTS 26

Search completed: May 29, 2003, 10:36:22  
 Job time : 21.333 secs

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GenCov version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:33:36 / Search time 7.2381 Seconds

(without alignments)  
65,040 Million cell updates/sec

Title: US-09-147-362a-9

Sequence: 1 LLSWGCKGRVLYCTS 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 2942292 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents: AA\*

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5: /cgn2\_6/prodata/1/isa/6C\_COMB.pep.\*

6: /cgn2\_6/prodata/1/isa/backfiller.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	96.7	33	4	US-09-433-4280-6
2	88	96.7	33	4	US-09-433-4280-5
3	88	96.7	40	3	US-08-894-639-35
4	88	96.7	40	3	US-08-894-639-36
5	88	96.7	40	3	US-08-444-410-39
6	88	96.7	40	4	US-09-444-410-68
7	86	94.5	33	4	US-09-433-4280-30
8	86	94.5	40	3	US-08-894-639-36
9	86	94.5	40	4	US-09-444-410-36
10	85	93.4	33	4	US-09-433-4280-20
11	85	93.4	40	3	US-08-894-639-41
12	85	93.4	40	3	US-08-894-639-42
13	82	90.1	23	4	US-09-433-4280-68
14	82	90.1	33	4	US-09-433-4280-4
15	82	90.1	33	4	US-09-433-4280-7
16	82	90.1	33	4	US-09-433-4280-15
17	82	90.1	37	4	US-08-817-441-86
18	82	90.1	37	4	US-08-894-639-69
19	82	90.1	41	3	US-08-894-639-69
20	82	90.1	42	3	US-08-894-639-66
21	82	90.1	42	4	US-09-444-410-66
22	82	90.1	200	4	US-08-865-056-104
23	81	89.0	23	4	US-09-433-4280-59
24	81	89.0	23	4	US-09-433-4280-60
25	81	89.0	23	4	US-08-433-4280-61
26	81	89.0	23	4	US-08-433-4280-62
27	81	89.0	28	4	US-09-433-4280-62

28	81	89.0	30	4	US-09-433-4280-63	Sequence 63, Appl
29	81	89.0	33	4	US-09-433-4280-5	Sequence 5, Appl
30	81	89.0	33	4	US-09-433-4280-5	Sequence 5, Appl
31	81	89.0	33	4	US-09-433-4280-14	Sequence 14, Appl
32	81	89.0	33	4	US-09-433-4280-16	Sequence 16, Appl
33	81	89.0	33	4	US-09-433-4280-29	Sequence 29, Appl
34	81	89.0	35	4	US-08-933-4280-64	Sequence 64, Appl
35	81	89.0	41	3	US-08-894-639-67	Sequence 67, Appl
36	81	89.0	41	3	US-08-894-639-67	Sequence 67, Appl
37	81	89.0	149	4	US-09-433-4280-67	Sequence 67, Appl
38	81	89.0	149	4	US-09-433-4280-67	Sequence 67, Appl
39	81	89.0	215	2	US-08-912-129A-58	Sequence 58, Appl
40	81	89.0	220	4	US-09-433-4280-66	Sequence 66, Appl
41	81	89.0	245	2	US-08-912-129A-48	Sequence 48, Appl
42	81	89.0	368	4	US-09-433-4280-58	Sequence 58, Appl
43	81	89.0	373	2	US-08-912-129A-52	Sequence 52, Appl
44	81	89.0	439	4	US-09-433-4280-57	Sequence 57, Appl
45	81	89.0	460	2	US-08-912-129A-60	Sequence 60, Appl

## ALIGNMENTS

```

RESULT 1
US-09-433-4280-6
Sequence 6, Application US/094334280
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
CURRENT APPLICATION NUMBER: US/09/433/4280
NUMBER OF SEQ ID NOS: 11-04
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 6
LENGTH: 33
TYPE: PRT
ORIGINISM: Human immunodeficiency virus type 1
US-09-433-4280-6
Query Match
Best Local Similarity 96.7% Score 89, DB 4, Length 33,
Matches 15, Conservative 1, Mismatches 0, Indels 0, Gaps 0,
1 LLSWGCKGRVLYCTS 16
14 LLSWGCKGRVLYCTS 29
RESULT 2
US-09-433-4280-25
Sequence 25, Application US/094334280
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
CURRENT APPLICATION NUMBER: US/09/433/4280
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 25
LENGTH: 33
TYPE: PRT
ORIGINISM: Human immunodeficiency virus type 1
US-09-433-4280-25
Query Match
Best Local Similarity 93.8% Pred. No. 4.3e-07,
Matches 15, Conservative 1, Mismatches 0, Indels 0, Gaps 0,

```

Qy 1 LLSWCGCKRGLVCYTS 16  
 ||:|||||  
 Db 14 LLSWCGCKRGLVCYTS 29

## RESULT 3

US-08-894-699-39  
 Sequence 39 Application US/08894699  
 Patent No. 6030769

## GENERAL INFORMATION:

APPLICANT: SARAGOSTI, SIMON, FRANCOIS  
 APPLICANT: LOUSBERT-AJAKA, IBITISSAM  
 APPLICANT: LY, THOI-DUONG  
 APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESSES:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 STREET: 175 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA

## COMPUTER READABLE FORM:

OPERATING SYSTEM: IBM PC COMPATIBLE  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 FILING DATE: 01-DEC-1997  
 PCT/FR96/00294

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/00294  
 FILING DATE: 26-FEB-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614

## REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000

INVENTOR FOR SEQ ID NO: 39:  
 SEQUENTIAL ORDER

LENGTH: 40 amino acids  
 TYPE: amino acid  
 STANDARDS: single

TOPOLOGY: linear  
 MOLECULE TYPE: peptide

US-08-894-699-39  
 Query Match 96.7%; Score 88; DB 3; Length 40;  
 Best Local Similarity 93.8%; Pred. No. 5,2e-07;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLSWCGCKRGLVCYTS 16  
 ||:|||||  
 Db 19 LLSWCGCKRGLVCYTS 34

## RESULT 4

US-08-894-699-68  
 Sequence 68 Application US/08894699  
 Patent No. 6030769

## GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS  
 APPLICANT: SARAGOSTI, SIMON, FRANCOIS  
 APPLICANT: LOUSBERT-AJAKA, IBITISSAM  
 APPLICANT: LY, THOI-DUONG  
 APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESSES:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 STREET: 175 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA

## COMPUTER READABLE FORM:

OPERATING SYSTEM: IBM PC COMPATIBLE  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 FILING DATE: 01-DEC-1997  
 PCT/FR96/00294

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/00294  
 FILING DATE: 26-FEB-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614

## REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000

INFORMATION FOR SEQ ID NO: 68:  
 LENGTH: 40 amino acids  
 TYPE: amino acid  
 STANDARDS: single

TOPOLOGY: linear  
 MOLECULE TYPE: peptide

US-08-894-699-68  
 Query Match 96.7%; Score 88; DB 3; Length 40;  
 Best Local Similarity 93.8%; Pred. No. 5,2e-07;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLSWCGCKRGLVCYTS 16  
 ||:|||||  
 Db 19 LLSWCGCKRGLVCYTS 34

## RESULT 5

US-09-444-410-39  
 Sequence 39 Application US/09444410  
 Patent No. 6270975

## GENERAL INFORMATION:

APPLICANT: SARAGOSTI, SIMON, FRANCOIS  
 APPLICANT: LOUSBERT-AJAKA, IBITISSAM  
 APPLICANT: LY, THOI-DUONG  
 APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
 TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESSES:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 STREET: 175 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA

```

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/894,699
FILING DATE:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-39

Query Match 96.7%; Score 88; DB 4; Length 40;
Best Local Similarity 93.8%; Pctd. No. 5,2e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

1 LLSWGCKGRIVCYTS 16
DB 19 LLSWGCKGRIVCYTS 34

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,410
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/894,699
FILING DATE:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-OPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-444-410-68

Query Match 96.7%; Score 88; DB 4; Length 40;
Best Local Similarity 93.8%; Pctd. No. 5,2e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

1 LLSWGCKGRIVCYTS 16
DB 19 LLSWGCKGRIVCYTS 34

RESULT 7
US-09-433-428D-30
Sequence 30, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
APPLICANT: LOUSSERTI-ADANA, IBTISSEM
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 30
LENGTH: 33
TYPE: PPT
ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-30

Query Match 94.5%; Score 86; DB 4; Length 33;
Best Local Similarity 87.5%; Pctd. No. 8,7e-07;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0.

1 LLSWGCKGRIVCYTS 16
DB 14 LLSWGCKGRIVCYTS 29

RESULT 8
US-08-894-699-36
Sequence 36, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: LOUSSERTI-ADANA, IBTISSEM
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/08/894,699
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 36
LENGTH: 33
TYPE: PPT
ORGANISM: Human immunodeficiency virus type 1
US-08-894-699-36

```

TITLE OF INVENTION: GROUP O HIV-1 FRAGMENTS OF SUCH  
 TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ADDRESS: P.C.  
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/894,699  
 FILING DATE: 01-DEC-1997  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/FR96/00294  
 PRIOR APPLICATION DATA: 1996  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 40 amino acids  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-894-699-36

Query Match 94.5% Score 86; DB 3; Length 40;  
 Best Local Similarity 87.5%; Pred. No. 1e-06;  
 Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 LLSNGCKGRIVCYTS 16  
 19 LLSNGCKGRIVCYTS 34

RESULT 9  
 US-09-444-410-36  
 ; Sequence 36: Application US/09444410  
 ; Patent No. 6270975  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SIMON, FRANCOIS  
 ; APPLICANT: SARAGOSTI, SENIOR  
 ; APPLICANT: LOUSSET-ADANA, IBTISSEM  
 ; APPLICANT: CHAÏA-BANDIER, MARIE-LAURE  
 ; TITLE OF INVENTION: GROUP O HIV-1 FRAGMENTS OF SUCH  
 ; TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ; ADDRESS: P.C.  
 ; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 ; CITY: ARLINGTON  
 ; STATE: VA  
 ; COUNTRY: USA

ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/444,410  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/894,699  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 40 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-444-410-36

Query Match 94.5% Score 86; DB 4; Length 40;  
 Best Local Similarity 87.5%; Pred. No. 1e-06;  
 Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 LLSNGCKGRIVCYTS 16  
 19 LLSNGCKGRIVCYTS 34

Db 19 LLSNGCKGRIVCYTS 34

RESULT 10  
 US-09-433-428D-20  
 ; Sequence 20: Application US/09433428D  
 ; Patent No. 6149310  
 ; GENERAL INFORMATION:  
 ; APPLICANT: De Looz, Robert J.  
 ; APPLICANT: Zhang, Jien  
 ; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
 ; FILE REFERENCE: CDS-207  
 ; CURRENT APPLICATION NUMBER: US/09/433,428D  
 ; CURRENT FILING DATE: 1999-11-04  
 ; INVENTOR: P. SEQ ID NOS: 70  
 ; SOFTWARE: PatentIn ver. 2.0  
 ; SEQ ID NO 20  
 ; LENGTH: 33  
 ; TYPE: PPT  
 ; ORGANISM: Human immunodeficiency virus type 1  
 ; US-09-433-428D-20

Query Match 93.4% Score 85; DB 4; Length 33;  
 Best Local Similarity 93.8%; Pred. No. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 LLSNGCKGRIVCYTS 16  
 14 LLSNGCKGRIVCYTS 29

Db 14 LLSNGCKGRIVCYTS 29

RESULT 11  
 US-08-894-699-41  
 ; Sequence 41: Application US/08894699  
 ; Patent No. 6030769

GENERAL INFORMATION:  
 APPLICANT: SIMON, FRANCOIS  
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION NUMBER: US/08/894,699  
 FILING DATE: 01-DEC-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/FR96/00294  
 FILING DATE: 26-FEB-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 NAME: OSLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 41:  
 SEQUENCE CHARACTERISTICS  
 LENGTH: 40 amino acids  
 TYPE: amino acid  
 STRAIDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-894-699-41

Query Match 93.4%, Score 85, DB 3, Length 40;  
 Best Local Similarity 93.8%, Pred. No. 1, 5e-06;  
 Matches 15, Conservative 0, Mismatches 1, Indels 0, Gaps 0;

Db 19 LLSWGCKGRIVCYTS 34

RESULT 12  
 US-09-444-410-41  
 Sequence 41, Application US/09444410  
 Patent No. 6270975  
 GENERAL INFORMATION:  
 APPLICANT: SIMON, FRANCOIS  
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION NUMBER: US/08/894,699  
 FILING DATE: 01-DEC-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/FR96/00294  
 FILING DATE: 26-FEB-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 NAME: OSLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 41:  
 SEQUENCE CHARACTERISTICS  
 LENGTH: 40 amino acids  
 TYPE: amino acid  
 STRAIDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-894-699-41

ADDRESSER: P.C.  
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION NUMBER: US/09/444,410  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/894,699  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/02236  
 FILING DATE: 27-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OSLON, NORMAN F.  
 REGISTRATION NUMBER: 24,614  
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 41:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 40 amino acids  
 TYPE: amino acid  
 STRAIDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-444-410-41

Query Match 93.4%, Score 85, DB 4, Length 40;  
 Best Local Similarity 93.8%, Pred. No. 1, 5e-06;  
 Matches 15, Conservative 0, Mismatches 1, Indels 0, Gaps 0;

Db 19 LLSWGCKGRIVCYTS 34

RESULT 13  
 US-09-433-428D-68  
 Sequence 68 Application US/09433428D  
 Patent No. 6149375  
 GENERAL INFORMATION:  
 APPLICANT: De Lays, Robert J.  
 TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
 FILE REFERENCE: CDS-207  
 CURRENT APPLICATION NUMBER: US/09/433,428D  
 FILING DATE: 1993-11-04  
 NUMBER OF SEQ ID NOS: 70  
 SOFTWARE: Patent Ver. 2.0  
 SEQ ID NO 68  
 LENGTH: 23  
 TYPE: PRT  
 ORIGINISM: Human immunodeficiency virus type 1  
 US-09-433-428D-68

Query Match 90.1%, Score 82, DB 4, Length 23;  
 Best Local Similarity 87.5%, Pred. No. 2, 5e-06;  
 Matches 14, Conservative 1, Mismatches 1, Indels 0, Gaps 0;

Db 4 LLSWGCKGRIVCYTS 19

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RESULT 14
US-09-433-428D-1
; Sequence 1, Application US/09433428D
; Sequence No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leyn, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 1
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; US-433-428D-1
Query Match
Best Local Similarity 90.1%, Score 82, DB 4, Length 33,
Matches 14, Conservative 1, Mismatches 1, Indels 0;
Oy 1 LLSWCGCKGRIVCYTS 16
Db 14 LLSWCGCKGRIVCYTS 29

RESULT 15
US-09-433-428D-4
; Sequence 4, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leyn, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 4
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; US-433-428D-4
Query Match
Best Local Similarity 90.1%, Score 82, DB 4, Length 33,
Matches 14, Conservative 1, Mismatches 1, Indels 0;
Oy 1 LLSWCGCKGRIVCYTS 16
Db 14 LLSWCGCKGRIVCYTS 29

Search completed: May 29, 2003, 10:41:28
Job time : 7.2381 secs
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GenCorp version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OK protein - protein search, using sw model

Run on: May 29, 2003, 10:39:21 | Search time 13.9413 Seconds

(Without alignments)  
117,011 Million cell updates/sec

Title: US-09-147-362a-9

Perfect score: 91

Sequence: 1 LLSWGCKGLVCTYS 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 383519 seqs, 10123694 residues

1 number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter: 45 summaries

Database:

Published Applications AA:  
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2: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
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11: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/prodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
14: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep.\*

Prod No. is the number of results predicted by chance to have a score at least as high as the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	82	90.1	200	10	US-10-026-741-66
2	82	90.1	200	10	US-09-854-816-104
3	81	89.0	215	1	US-08-911-824-56
4	81	89.0	245	1	US-08-911-824-48
5	81	89.0	281	1	US-08-911-824-120
6	81	89.0	373	1	US-08-911-824-52
7	81	89.0	460	1	US-08-911-824-60
8	81	89.0	490	1	US-08-911-824-55
9	81	89.0	526	1	US-08-911-824-97
10	81	89.0	618	1	US-08-911-824-93
11	81	89.0	706	1	US-08-911-824-91
12	81	89.0	736	1	US-08-911-824-91
13	81	89.0	973	1	US-08-911-824-61
14	81	89.0	973	1	US-08-911-824-61
15	81	89.0	973	1	US-08-911-824-61
16	81	89.0	973	1	US-08-911-824-61
17	79	86.8	224	9	US-10-059-271-87
18	79	86.8	256	9	US-10-059-271-97
19	79	86.8	256	9	US-10-059-271-97

20	78	85.7	213	10	US-09-854-816-103	Sequence 103, App
21	76	83.5	222	9	US-10-059-271-77	Sequence 7, App1
22	75	82.4	35	9	US-10-026-741-101	Sequence 101, App
23	75	82.4	35	9	US-10-026-741-101	Sequence 101, App
24	75	82.4	37	9	US-10-026-741-90	Sequence 97, App1
25	75	82.4	351	9	US-10-026-741-47	Sequence 47, App1
26	75	82.4	877	9	US-10-026-741-102	Sequence 102, App1
27	74	81.3	23	9	US-09-188-847-4	Sequence 2, App1
28	74	81.3	23	12	US-10-000-321-2	Sequence 2, App1
29	74	81.3	35	9	US-08-886-156-62	Sequence 62, App1
30	74	81.3	35	9	US-08-886-156-62	Sequence 62, App1
31	74	81.3	35	9	US-08-886-156-62	Sequence 62, App1
32	74	81.3	35	9	US-08-886-156-62	Sequence 62, App1
33	74	81.3	37	9	US-09-886-153-62	Sequence 88, App1
34	74	81.3	146	12	US-10-000-321-105	Sequence 105, App1
35	74	81.3	204	10	US-09-854-816-105	Sequence 105, App1
36	74	81.3	351	9	US-08-886-156-66	Sequence 46, App1
37	74	81.3	351	9	US-08-886-156-66	Sequence 46, App1
38	74	81.3	351	9	US-08-886-156-66	Sequence 46, App1
39	74	81.3	351	9	US-08-886-156-66	Sequence 46, App1
40	70	76.9	24	9	US-10-026-741-34	Sequence 34, App1
41	70	76.9	29	9	US-10-026-741-33	Sequence 33, App1
42	70	76.9	37	9	US-10-026-741-94	Sequence 94, App1
43	70	76.9	104	9	US-10-026-741-100	Sequence 100, App
44	70	76.9	121	9	US-10-059-271-84	Sequence 84, App1
45	68	74.7	22	9	US-10-059-271-5	Sequence 5, App1

## ALIGNMENTS

RESULT 1  
US-09-854-816-103  
Sequence 86, App1  
Publication No.: US20010049604A1  
GENERAL INFORMATION:  
APPLICANT: CHARNEAU, PIERRE  
CLAVEL, FRANCOISE  
BOWMAN, ANDREW  
QUILLIENT, CAROLINE  
MONTIGNIER, ENRIQUE  
DONZON DE SAINT-MARTIN, JACQUELINE  
COHEN, JAVOES  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE 1OR  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DUNNIGAN, Henderson, Fairbow, Garrett &  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.10  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/026-741  
FILING DATE: 27-Dec-2001  
PRIORITY APPLICATION NUMBER: US 08/817,441  
FILING DATE: 31-AUG-1998  
APPLICATION NUMBER: PCT/FR 95/01391  
FILING DATE: 20-OCT-1995  
APPLICATION NUMBER: FR 9412554  
FILING DATE: 20-OCT-1994  
PRIORITY APPLICATION NUMBER: FR 93-1835  
FILING DATE: 01-MAR-1993  
ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 03260,6005-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 86:  
 SEQUENCE CHARACTERISTICS:  
 TYPE: amino acid acids  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 86:  
 US-10-026-741-86

Query Match  
 Best Local Similarity 90.1%; Score 82; DB 9; Length 37;  
 Matches 14; Conservative 1; Mismatches 1; Indels 0;  
 Gaps 0;

DB 14 LLSWGCKGRIVCYTS 29

RESULT 2  
 US-09-854-816-104  
 Sequence 104, Application US/09854816  
 Patent No. US20020151473A1  
 GENERAL INFORMATION:  
 APPLICANT: NEWCOW C. Brasted  
 J. Kevin Judice  
 Robert S. McDowell  
 J. Christopher Phelan  
 James A. Stavovskikh  
 Melissa A. Wells  
 TITLE OF INVENTION: Correlated helical peptides and methods of  
 NUMBER OF SEQUENCES: Making Same  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94020  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Winpatin (Genentech)  
 CURRENT APPLICATION DATA: US/09/854, 816  
 FILING DATE: 15-MAY-2003  
 CLASSIFICATION: <unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/965,056  
 FILING DATE: <unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: J. Christopher Phelan  
 REGISTRATION NUMBER: 36,700  
 REFERENCE/DOCKET NUMBER: P100502  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-8674  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 104:  
 SEQUENCE CHARACTERISTICS:  
 TYPE: amino acid acids  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 104:  
 US-09-854-816-104

Query Match  
 Best Local Similarity 89.1%; Score 81; DB 10; Length 200;  
 Matches 14; Conservative 1; Mismatches 1; Indels 0;  
 Gaps 0;

DB 126 LLSWGCKGRIVCYTS 141

RESULT 3  
 US-08-911-824-58  
 Sequence 58, Application US/08911824  
 Publication No. US2003004323A1  
 GENERAL INFORMATION:  
 APPLICANT: Abbott Laboratories  
 APPLICANT: Abbott, John R., Jr.  
 APPLICANT: Yamaguchi, Julie  
 APPLICANT: Golden, Alan M.  
 APPLICANT: Brennan, Catherine A.  
 APPLICANT: Hickman, Robert K.  
 APPLICANT: Devare, Sushil G.  
 TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
 PREVENTION OF HIV INFECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV  
 FILE REFERENCE: 6145 US 01  
 CURRENT APPLICATION NUMBER: US/08/911, 824  
 CURRENT FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 121  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO: 58  
 LENGTH: 215  
 TYPE: PPT  
 ORGANISM: Human Immunodeficiency Virus  
 FEATURE:  
 OTHER INFORMATION: Encodes recombinant protein pCO-8PL  
 US-08-911-824-58

Query Match  
 Best Local Similarity 89.0%; Score 81; DB 1; Length 215;  
 Matches 13; Conservative 1; Mismatches 1; Indels 0;  
 Gaps 0;

DB 127 LLSWGCKGRIVCYTS 142

RESULT 4  
 US-08-911-824-48  
 Sequence 48, Application US/08911824  
 Publication No. US2003004323A1  
 GENERAL INFORMATION:  
 APPLICANT: Abbott Laboratories  
 APPLICANT: Abbott, John R., Jr.  
 APPLICANT: Yamaguchi, Julie  
 APPLICANT: Golden, Alan M.  
 APPLICANT: Brennan, Catherine A.  
 APPLICANT: Hickman, Robert K.  
 APPLICANT: Devare, Sushil G.  
 TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
 PREVENTION OF HIV INFECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV  
 FILE REFERENCE: 6145 US 01  
 CURRENT APPLICATION NUMBER: US/08/911, 824  
 CURRENT FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 121  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO: 48  
 LENGTH: 245  
 TYPE: PPT  
 ORGANISM: Human Immunodeficiency Virus  
 FEATURE:  
 OTHER INFORMATION: Encodes recombinant protein pCO-9PL  
 US-08-911-824-48

Query Match  
 Best Local Similarity 89.0%; Score 81; DB 1; Length 245;  
 Matches 13; Conservative 1; Mismatches 1; Indels 0;  
 Gaps 0;

Best Local Similarity 81.2%; Pred. No. 0.000113;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 L1SSWGCKGR1CYTTS 16  
Db 127 L1N1WGCKGR1CYTTS 142

## RESULT 5

US-08-911-824-120  
Sequence 120, Application US/08911824  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Yaeguchi, Julie  
APPLICANT: Goldman, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Devare, Sushil G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165.US.O1 US/08/911,824  
CURRENT FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 120  
LENGTH: 281  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: Encodes recombinant protein pCO-15PL  
US-08-911-824-120

Query Match 89.0%; Score 81; DB 1; Length 281;  
Best Local Similarity 81.2%; Pred. No. 0.00014;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 L1SSWGCKGR1CYTTS 16  
Db 127 L1N1WGCKGR1CYTTS 142

## RESULT 6

US-08-911-824-52  
Sequence 95, Application US/08911824  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Yaeguchi, Julie  
APPLICANT: Goldman, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Devare, Sushil G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165.US.O1 US/08/911,824  
CURRENT FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 52  
LENGTH: 373  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: Encodes recombinant protein pCO-11PL  
US-08-911-824-52

Query Match 89.0%; Score 81; DB 1; Length 373;  
Best Local Similarity 81.2%; Pred. No. 0.00018;

Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 L1SSWGCKGR1CYTTS 16  
Db 127 L1N1WGCKGR1CYTTS 142

## RESULT 7

US-08-911-824-60  
Sequence 60, Application US/08911824  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Yaeguchi, Julie  
APPLICANT: Goldman, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Devare, Sushil G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165.US.O1 US/08/911,824  
CURRENT FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 60  
LENGTH: 460  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: Encodes recombinant protein pCO-8CKS  
US-08-911-824-60

Query Match 89.0%; Score 81; DB 1; Length 460;  
Best Local Similarity 81.2%; Pred. No. 0.00022;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 L1SSWGCKGR1CYTTS 16  
Db 372 L1N1WGCKGR1CYTTS 387

## RESULT 8

US-08-911-824-95  
Sequence 95, Application US/08911824  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Yaeguchi, Julie  
APPLICANT: Goldman, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Devare, Sushil G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165.US.O1 US/08/911,824  
CURRENT FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 95  
LENGTH: 488  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: Encodes recombinant protein pCO-14PL  
US-08-911-824-95

Query Match 89.0%; Score 81; DB 1; Length 488;  
Best Local Similarity 81.2%; Pred. No. 0.00023;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 L15SGCKGR1CYTS 16  
||:|||||:  
Db 127 L15SGCKGR1CYTS 142

RESULT 9  
US-08-911-824-50  
Sequence 57: Application US/08911824  
Publication No. US20030004323A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Yamaguchi, Julie  
APPLICANT: Golden, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Deware, Shelli G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165 US.O1  
CURRENT APPLICATION NUMBER: US/08/911,824  
CURRENT FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 127  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 50  
LENGTH: 490  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: Encodes recombinant protein pCO-9CKS  
US-08-911-824-50  
Query Match 89.0%; Score 81; DB 1; Length 490;  
Best Local Similarity 81.2%; Pred. No. 0.00023;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Cy 1 L15SGCKGR1CYTS 16  
||:|||||:  
Db 372 L15SGCKGR1CYTS 387

RESULT 10  
US-08-911-824-97  
Sequence 57: Application US/08911824  
Publication No. US20030004323A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Yamaguchi, Julie  
APPLICANT: Golden, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Deware, Shelli G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165 US.O1  
CURRENT APPLICATION NUMBER: US/08/911,824  
CURRENT FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 97  
LENGTH: 526  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: Encodes recombinant protein pCO-15CKS  
US-08-911-824-97  
Query Match 89.0%; Score 81; DB 1; Length 526;  
Best Local Similarity 81.2%; Pred. No. 0.00025;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 L15SGCKGR1CYTS 16  
||:|||||:  
Db 372 L15SGCKGR1CYTS 387

RESULT 11  
US-08-911-824-54  
Sequence 57: Application US/08911824  
Publication No. US20030004323A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Yamaguchi, Julie  
APPLICANT: Golden, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Deware, Shelli G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165 US.O1  
CURRENT APPLICATION NUMBER: US/08/911,824  
CURRENT FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 127  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 54  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: Encodes recombinant protein pCO-11CKS  
US-08-911-824-54  
Query Match 89.0%; Score 81; DB 1; Length 618;  
Best Local Similarity 81.2%; Pred. No. 0.00028;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Cy 1 L15SGCKGR1CYTS 16  
||:|||||:  
Db 372 L15SGCKGR1CYTS 387

RESULT 12  
US-08-911-824-93  
Sequence 93: Application US/08911824  
Publication No. US20030004323A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Yamaguchi, Julie  
APPLICANT: Golden, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Deware, Shelli G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165 US.O1  
CURRENT APPLICATION NUMBER: US/08/911,824  
CURRENT FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 93  
LENGTH: 706  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: Encodes recombinant protein pCO-13CKS  
US-08-911-824-93  
Query Match 89.0%; Score 81; DB 1; Length 706;  
Best Local Similarity 81.2%; Pred. No. 0.00022;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Cy 1 L15SGCKGR1CYTS 16  
||:|||||:  
Db 372 L15SGCKGR1CYTS 387

Db 618 L1M1MGCKGR1CYTS 633

RESULT 13  
US-08-911-824-91

Sequence 91: Application US/08911824  
Publication No. US20030004323A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Vamaguchi, Julie  
APPLICANT: Golden, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Devare, Sushil G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165 US 01  
CURRENT FILING DATE: 1997-08-15  
CURRENT APPLICATION NUMBER: US/08/911,824  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatSeq for Windows Version 3.0  
SEQ ID NO 91  
LENGTH: 736  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: Encodes recombinant protein pCO-12CKS  
US-08-911-824-91

Query Match 89.0%, Score 81; DB 1; Length 736;  
Best Local Similarity 81.2%; Pred. No. 0.00031;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Oy 1 L1M1MGCKGR1CYTS 16  
Db 618 L1M1MGCKGR1CYTS 633

RESULT 14  
US-08-911-824-61  
Sequence 61: Application US/08911824  
Publication No. US20030004323A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Hackett, John R., Jr.  
APPLICANT: Vamaguchi, Julie  
APPLICANT: Golden, Alan M.  
APPLICANT: Brennan, Catherine A.  
APPLICANT: Hickman, Robert K.  
APPLICANT: Devare, Sushil G.  
TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE  
FILE REFERENCE: 6165 US 01  
CURRENT FILING DATE: 1997-08-15  
CURRENT APPLICATION NUMBER: US/08/911,824  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatSeq for Windows Version 3.0  
SEQ ID NO 61  
LENGTH: 873  
TYPE: PRT  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
OTHER INFORMATION: HIV-1 Group O isolate HAM12  
US-08-911-824-61

Query Match 89.0%, Score 81; DB 1; Length 873;  
Best Local Similarity 81.2%; Pred. No. 0.00038;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Oy 1 L1M1MGCKGR1CYTS 16

Db 601 L1M1MGCKGR1CYTS 616

RESULT 15  
US-10-059-271-6  
Sequence 6: Application US/10059271  
Publication No. US20030082208A1  
GENERAL INFORMATION:  
APPLICANT: REBE, HEINRICH  
APPLICANT: RUDE, REINHARD  
APPLICANT: KREIBER, ANDREAS  
TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPIC SEQUENCES AND  
FILE REFERENCE: ALBER-22  
CURRENT FILING DATE: 2002-01-31  
CURRENT APPLICATION NUMBER: US/10/059,271  
PRIOR APPLICATION NUMBER: DE 101 06 295  
CURRENT FILING DATE: 2001-02-02  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatSeq Ver. 2.1  
SEQ ID NO 6  
LENGTH: 22  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-059-271-6

Query Match 86.8%, Score 79; DB 9; Length 22;  
Best Local Similarity 81.2%; Pred. No. 3.1e-05;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Oy 1 L1M1MGCKGR1CYTS 16  
Db 7 L1M1MGCKGR1CYTN 22

Search completed: May 29, 2003, 11:03:58  
Job time: 14.8413 secs

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C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #ext\_change 12-Apr-1995  
 C:Accession: S22000  
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 A:Submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi  
 A:Reference number: S21990  
 A:Accession: S22000  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STE2>  
 A:Cross-references: EMBL:X61351  
 C:Superfamily: type E retrovirus env polypeptin

Query Match 68.1%; Score 62; DB 2; Length 357;  
 Best Local Similarity 66.7%; Pred. No. 0.048;  
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRVLCYT 15  
 94 LGLWGCKGRVLCYT 108

RESULT 8  
 S22000 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: patient 3B  
 C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #ext\_change 26-Aug-1999  
 C:Accession: S70417  
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 A:IDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70417  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-358 <STE2>  
 A:Cross-references: EMBL:X61351; NID:960184; PIND:CA43614.1; PID:960185  
 C:Superfamily: type E retrovirus env polypeptin

Query Match 68.1%; Score 62; DB 2; Length 358;  
 Best Local Similarity 66.7%; Pred. No. 0.048;  
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRVLCYT 15  
 94 LGLWGCKGRVLCYT 108

RESULT 9  
 S22000 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4U)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #ext\_change 26-Aug-1999  
 C:Accession: S70420; S22006  
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 A:IDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70420  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STE2>  
 A:Cross-references: EMBL:X61351; NID:960190; PIND:CA43620.1; PID:960191  
 A:Superfamily: type E retrovirus env polypeptin

Query Match 65.9%; Score 60; DB 2; Length 357;  
 Best Local Similarity 56.2%; Pred. No. 0.096;  
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRVLCYT 15  
 94 LGLWGCKGRVLCYT 108

DB 93 LGLWGCKGRVLCYT 108

RESULT 10  
 S21994 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 2B  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #ext\_change 01-Dec-2000  
 C:Accession: S21994; S70421; S70422  
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 A:Submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi  
 A:Reference number: S21990  
 A:Accession: S21994  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STE2>  
 A:Cross-references: EMBL:X61355; NID:960179; PIND:CA43622.1; PID:960180  
 A:IDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70421  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STE2>  
 A:Cross-references: EMBL:X61355; NID:960179  
 C:Superfamily: type E retrovirus env polypeptin

Query Match 65.9%; Score 60; DB 2; Length 357;  
 Best Local Similarity 56.2%; Pred. No. 0.096;  
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRVLCYT 15  
 93 LGLWGCKGRVLCYT 108

RESULT 11  
 S22000 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 4B  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #ext\_change 01-Dec-2000  
 C:Accession: S22004; S70419  
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 A:Submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi  
 A:Reference number: S22004  
 A:Accession: S22004  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STE2>  
 A:Cross-references: EMBL:X61353; NID:960188; PIND:CA43618.1; PID:960189  
 A:IDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70419  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STE2>  
 A:Cross-references: EMBL:X61353; NID:960188  
 C:Superfamily: type E retrovirus env polypeptin

Query Match 65.9%; Score 60; DB 2; Length 357;  
 Best Local Similarity 56.2%; Pred. No. 0.096;  
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LLSWGCKGRVLCYT 15  
 93 LGLWGCKGRVLCYT 108

```

RESULT 12
521996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
R:Steuiler, H., Storch-Hagenlocher, B., Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by polymerase chain reaction
A:Accession number: S70417; M01D:92144209; PMID:1736940
A:Accession: S70422
A>Status: preliminary
A:Molecule type: DNA
A:Cross-references: EMBL:X61356; NID:660181; PIDN:CA416324.1; PID:g1067129
A:Experimental source: patient 27L
A>Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein

Query Match 65.94% Score 60; DB 2; Length 357;
Ident. Local Similarity 56.24% Pred. No. 0.096; Gaps 0;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 LLSWGGCKGRIVCYTS 16
|| ||| ||| ||| |||
Db 93 LGLWGSGSKLICTTN 108

RESULT 13
521997
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
R:Steuiler, H., Storch-Hagenlocher, B., Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by polymerase chain reaction
A:Accession number: S70417; M01D:92144209; PMID:1736940
A:Reference number: S70417; M01D:92144209; PMID:1736940
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by polymerase chain reaction
A:Molecule type: DNA
A>Status: preliminary
A:Cross-references: EMBL:X61358; NID:660177; PIDN:CA416328.1; PID:g60178
A:Experimental source: patient 22
A>Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein

Query Match 65.94% Score 60; DB 2; Length 357;
Ident. Local Similarity 56.24% Pred. No. 0.096; Gaps 0;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 LLSWGGCKGRIVCYTS 16
|| ||| ||| ||| |||
Db 93 LGLWGSGSKLICTTN 108

RESULT 14
521998
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
R:Steuiler, H., Storch-Hagenlocher, B., Wildemann, B., Hacke, W.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by polymerase chain reaction
A:Accession number: S21998
A:Accession: S21998
A:Molecule type: DNA
A:Residues: 1-358 <67E>
A:Cross-references: EMBL:X61359; NID:660182; PIDN:CA416330.1; PID:g60183
A:Steuiler, H., Storch-Hagenlocher, B., Wildemann, B.

```

[illegible]

GenCode version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:31:50 / Search time 3.93651 Seconds

Title: US-09-147-362a-9 (without alignments)  
Sequence: 1 L155WQCKRLVCTYS 16  
168,581 Million cell updates/sec

Perfect score: 91  
Sequence: 1 L155WQCKRLVCTYS 16

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

1 number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database: SwissProt\_40.\*  
Lastering filter 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69.2	85.4	1	ENV_HV1CZ	P18040 human immunoprotease
2	68.9	84.7	1	ENV_HV1Y2	P15831 human immunoprotease
3	68.9	84.7	1	ENV_HV1S1	P15831 human immunoprotease
4	68.9	84.7	1	ENV_HV1M2	P15831 human immunoprotease
5	68.9	85.1	1	ENV_HV1B8	P04582 human immunoprotease
6	68.9	85.2	1	ENV_HV1B9	P12488 human immunoprotease
7	68.9	85.2	1	ENV_HV1B8	P12488 human immunoprotease
8	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
9	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
10	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
11	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
12	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
13	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
14	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
15	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
16	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
17	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
18	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
19	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
20	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
21	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
22	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
23	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
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27	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
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31	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
32	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease
33	68.9	85.1	1	ENV_HV1M2	P15831 human immunoprotease

34	55	60.4	85.1	1	ENV_HV2G1	P18040 human immunoprotease
35	55	60.4	85.1	1	ENV_HV2G1	P18040 human immunoprotease
36	55	60.4	85.1	1	ENV_HV2G1	P18040 human immunoprotease
37	55	60.4	85.1	1	ENV_HV2G1	P18040 human immunoprotease
38	55	60.4	85.1	1	ENV_HV2G1	P18040 human immunoprotease
39	55	60.4	85.1	1	ENV_HV2G1	P18040 human immunoprotease
40	55	60.4	85.1	1	ENV_HV2G1	P18040 human immunoprotease
41	55	60.4	85.1	1	ENV_HV2G1	P18040 human immunoprotease
42	55	60.4	85.1	1	ENV_HV2G1	P18040 human immunoprotease
43	55	60.4	85.1	1	ENV_HV2G1	P18040 human immunoprotease
44	55	60.4	85.1	1	ENV_HV2G1	P18040 human immunoprotease
45	55	60.4	85.1	1	ENV_HV2G1	P18040 human immunoprotease

## ALIGNMENTS

Result ID	ENV_HV1CZ	STANDARD	PRT	85.4 AA.
AC	P17281			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope polyprotein gp160 precursor [contamin: Exterior membrane glycoprotein (GP120), Transmembrane glycoprotein (GP41)].			
OS	Chimpanzee immunodeficiency virus (SIV/cp2) (CIV).			
CC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
CC	NCBI_TaxID=11723;			
RM	SEQUENCE FROM N.A.			
RM	MEHLING=9023077; PubMed=2188136;			
RM	Wang, J., Overbaugh, A., Roelants, G., Main-Hecken, S.,			
RM	"Genetic characterization of a chimpanzee lentivirus related to HIV-1."			
RM	Nature 345:356-359(1990).			
CC	-1- SIMILARITY: STRONG, WITH HIV-1 ENV POLYPROTEIN.			
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CC	EMBL: X52154; CA36407.1; -			
DR	PIR: S09990; VCIJST.			
DR	HIV: X52154; BMSV62.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00517; GP41.1.			
KW	Alts; Coat protein; Polypeptide; Glycoprotein; Transmembrane; SIGNAL.			
FT	CHAIN	1	30	
FT	CHAIN	31	600	
FT	CHAIN	501	600	
FT	TRANSMEM	675	693	
FT	TRANSMEM	805	821	
FT	CARBOHYD	134	134	
FT	CARBOHYD	140	140	
FT	CARBOHYD	143	143	
FT	CARBOHYD	154	154	
FT	CARBOHYD	154	154	
FT	CARBOHYD	186	186	
FT	CARBOHYD	195	195	
FT	CARBOHYD	239	239	
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FT	CARBOHYD	284	284	
FT	CARBOHYD	294	294	
FT	CARBOHYD	294	294	

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----- NOT ANNOTATED CDS.  
CC EMBU; M93258.;  
DR PIR; H44001; H44001;  
DR JALPRO; IPRO00726; BRY GP41.  
DR DRAMA; PRMO0517; Gpi20\_1.  
DR Pfam; PF00517; GP41; 1.  
KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane; signal.  
KM  
KV  
FT SIGNAL. 1 29  
FT CHAIN 30 459  
FT PROSITE PS00111 30 459  
FT TRANSMEM 730 752  
FT DISULFID 53 73  
FT FT DISULFID 118 201  
FT DISULFID 125 192  
FT DISULFID 130 155  
FT DISULFID 214 243  
FT BY SIMILARITY.  
BT BY SIMILARITY.

EXTERIOR MEMBRANE GLYCOPROTEIN.  
POSSIBLE EXTERIOR MEMBRANE GLYCOPROTEIN.  
BY SIMILARITY.  
BY SIMILARITY.  
BY SIMILARITY.  
BY SIMILARITY.  
BY SIMILARITY.

D7  
D8  
DT 01-FEB-1991 (Rel. 17, Created)  
DY 01-FEB-1991 (Rel. 17, Last sequence update)  
E1 DEB-1991 (Rel. 17, Deleted)

DE Evolutionary polypeptide g166 precursor [Contains: Exterior membrane glycoprotein (gp120), Transmembrane glycoprotein (gp41)]

G5 ENV.

GN Human immunodeficiency virus type 1 (SF662 isolate) (HIV-1).

OC Viruses; Retrocid viruses; Retroviridae; Lentivirus.  
OC 1101 Taxid:11691;

RX SEQUENCE FROM N.A.  
RX MEDLINE=90147855; PubMed=2849420;  
RA Cheng-Mayer C., Gutroga M., Tung J.W., Dina D., Levy J.;  
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism." Virology 1991;173(1):590-601.  
RT Collier AC et al. Cell 1992;69(3):1011-19.

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CN EMBL; MF65074; AAA45072.1; -



[illegible]

FT	DISULFID	376	439	BY SIMILARITY.
FT	DISULFID	383	412	N-LINKED (GLCNAC..)
FT	CARBOHYD	88	88	N-LINKED (GLCNAC..)
FT	CARBOHYD	135	135	N-LINKED (GLCNAC..)
FT	CARBOHYD	138	138	N-LINKED (GLCNAC..)
FT	CARBOHYD	154	154	N-LINKED (GLCNAC..)
FT	CARBOHYD	158	158	N-LINKED (GLCNAC..)
FT	CARBOHYD	157	157	N-LINKED (GLCNAC..)
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FT	CARBOHYD	442	442	N-LINKED (GLCNAC..)
FT	CARBOHYD	456	456	N-LINKED (GLCNAC..)
FT	CARBOHYD	607	607	N-LINKED (GLCNAC..)
FT	CARBOHYD	621	621	N-LINKED (GLCNAC..)
FT	CARBOHYD	633	633	N-LINKED (GLCNAC..)
FT	CARBOHYD	670	670	N-LINKED (GLCNAC..)
FT	CARBOHYD	812	812	N-LINKED (GLCNAC..)
SO	SEQUENCE	852 AA;	97203 MW;	28866345DEC915F CRIC64;

Query Match 65.9%; Score 60; DB 1; Length 852;  
 Best Local Similarity 56.2%; Pval No. 0.04;  
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 LLSWCGCRVAVCYTS 16  
 588 LLSWCGCRVAVCYTS 603

DB 01-FEB-1991 (Rel. 17, Created)  
 ID ENV\_HV1S3 STANDARD; PRT; 852 AA.  
 AC P19549;  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 ENVELOPE POLYPEPTIDE GP150 precursor [Contains: Exterior membrane glycoprotein (GP150); Transmembrane glycoprotein (GP41)].  
 OS ENV.  
 NCBI\_Taxid:11690;  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 SEQUENCE FROM N.A.  
 SOURCE: GenBank, accession: U00097.906;  
 RA York-Hislop D, Chomay-Mayer C, Bauer D, Levy J.A., Dina D;  
 RT "Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome." J. Virol. 64:4016-4020(1990).  
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 CC ENR1; M38427; M0045067.1.

DR	HIV; M38427; ENVSEF33.			
DR	Inter-Pro; IPR000328; Env GP41.			
DR	Inter-Pro; IPR000328; Env GP41.			
DR	PIfam; PF00516; GP120. 1.			
DR	PIfam; PF00516; GP120. 1.			
DR	PIfam; PF00516; GP120. 1.			
DR	PIfam; PF00516; GP120. 1.			
KW	Anti-CD4 protein; glycoprotein; gly			

Query Match	Score 60	DB 1	Length 853	Best Local Similarity 56.2%	Pred. No 0.04	Mismatches 9	Conservative 3	Indels 4	Gaps 0
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D8		590	LHGMCGSGGLCTTA	605
RESULT 9				
ENV_HVJ22				
AD	BKLVJ22	STANDARD:	PRT:	853 AA.
DT	01-OCT-1989 [Rel. 12, Created]			
DT	01-OCT-1989 [Rel. 12, Last sequence update]			
DT	16-OCT-2001 [Rel. 40, Last annotation update]			
D7	Envelope polyprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120), Transmembrane glycoprotein (GP41)].			
DN	ENV.			
OS	Human immunodeficiency virus type 1 (22/CDC-234 isolate) (HTV-1).			
CC	Nucleus; Retroviral viruses; Lentiviridae; Lentivirus.			
CC	[1] "taxid:11693".			
RN	SEQUENCE FROM N.A.			
RA	Theodore T., Buckler-Miller A.;			
RL	Submitted (NOV-1988) to the HIV data bank.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at Basel. The biological information contained here are contributions on which we have no copyright claim. This information may be used by others as long as it is modified and this statement is not removed. No charge by and for commercial entities requires a license agreement (see <a href="http://www.isdb.ch/announcements/">http://www.isdb.ch/announcements/</a> or send an email to <a href="mailto:license@isdb-sib.ch">license@isdb-sib.ch</a> ).			
CC	-----			
KW	EMBL, M22639; AAA45370.1; -			
DR	HIV_42639; ENV22Z6.			
DR	InterPro: IPR000775; GP120.			
DR	InterPro: PPO0516; GP120_1.			
KM	Pfam: PPO0516; GP41; 1.			
KA	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane signal.			
FT	SIGNAL	1	31	BY SIMILARITY.
FT	CHAIN	32	508	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	DISULFID	509	853	TRANSMEMBRAN GLYCOPROTEIN.
FT	DISULFID	118	206	BY SIMILARITY.
FT	DISULFID	125	197	BY SIMILARITY.
FT	DISULFID	130	154	BY SIMILARITY.
FT	DISULFID	219	248	BY SIMILARITY.
FT	DISULFID	229	240	BY SIMILARITY.
FT	DISULFID	297	330	BY SIMILARITY.
FT	DISULFID	376	442	BY SIMILARITY.
FT	DISULFID	381	455	BY SIMILARITY.
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FT	CARBOHYD	384	384	N-LINKED (GLCNAC . ) (POTENTIAL).
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FT	CARBOHYD	458	458	N-LINKED (GLCNAC . ) (POTENTIAL).





InterPro: IPR000777, GP120.  
 DR Pfam: PF00517, GP120.1.  
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM Signal.

FT SIGNAL 1 29  
 FT CHAIN 30 509  
 FT DISULFID 510 855  
 FT DISULFID 118 210  
 FT DISULFID 125 201  
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 FT DISULFID 223 252  
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 FT CARBOHYD 815 815  
 FT SEQUENCE 855 AA; 97476 MW; 567824607AD520H CAC64;

Query Match  
 at Local Similarity 56.2%; Score 60; DB 1; Length 855;  
 at Local Similarity 56.2%; Pred. No. 0.04; Mismatches 3; Indels 0; Gaps 0;

Db 1 LUSNCGKRLVCTYS 16  
 591 LADWSSKSLCTT 606

RESULT 12  
 ENV\_HV126 STANDARD; PRT; 855 AA.  
 NC 1045601.1987 [Rel. 05. Created]  
 NC 1045601.1987 [Rel. 05. Last sequence update]  
 DT 15-JUL-1999 [Rel. 38. Last annotation update]  
 DE Envelope POLYPEPTIDE GP120 precursor [Contains: Exterior membrane  
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 ON ENV.  
 ON Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).  
 ON NCBI\_GenBank:U01100; Retroviridae; Lentivirus.  
 CX [1]\_TaxID:11708;  
 RA Schöeteman G., Curran J., Kalyanaraman V.S., Luciw P.A.,  
 RP MEDLINE:87248097; PubMed:3036660;  
 RX Srinivasan A., Anand R., Ranganathan P., Feorino P.,  
 RA Schöeteman G., Curran J., Kalyanaraman V.S., Luciw P.A.,

Sanchez-Pescador R.;  
 Molecular characterization of human immunodeficiency virus from  
 RT domain in the envelope gene.  
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EMBL: X03456; AA45380.1;  
 F01: D26192; NCL25R.  
 DR InterPro: IPR000777, GP120.  
 DR InterPro: IPR000777, GP120.  
 DR Pfam: PF00517, GP120.1.  
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM Signal.

FT SIGNAL 1 29  
 FT CHAIN 30 509  
 FT DISULFID 511 855  
 FT DISULFID 118 207  
 FT DISULFID 125 198  
 FT DISULFID 220 249  
 FT DISULFID 238 332  
 FT DISULFID 378 444  
 FT DISULFID 385 417  
 FT CARBOHYD 87 87  
 FT CARBOHYD 129 129  
 FT CARBOHYD 140 140  
 FT CARBOHYD 145 145  
 FT CARBOHYD 152 152  
 FT CARBOHYD 158 158  
 FT CARBOHYD 186 186  
 FT CARBOHYD 189 189  
 FT CARBOHYD 199 199  
 FT CARBOHYD 236 236  
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 FT CARBOHYD 460 460  
 FT CARBOHYD 464 464  
 FT CARBOHYD 610 610  
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 FT CARBOHYD 673 673  
 FT SEQUENCE 855 AA; 384056239C345 CAC64;

Query Match  
 at Local Similarity 56.2%; Score 60; DB 1; Length 855;  
 at Local Similarity 56.2%; Pred. No. 0.04; Mismatches 3; Indels 0; Gaps 0;





Query Match 55.94; Score 60; DP 1; Length 856;  
Best Local Similarity 56.24; Pctd No. 0.04;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 ILSSWCKGRILVCTTS 16  
|||  
592 ILGLWGSRLICCTTA 607  
|||

Search completed: May 29, 2003, 10:36:59  
Job time : 3.93651 secs

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AC 0918B6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
OC Virus; Retroid viruses; Retroviridae; Lentivirus.
OS Human immunodeficiency virus type 1.
NCBI_TaxID=11676;
SEQUENCE FROM N.A.
RA Robert P., Robertson D., Sandrine S., Christel D., Francois S.,
RT Philippe M.;
RL "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
DR EMBL: AJ236404; CAB96282.1;
DR InterPro: IPR000328; ENV_GP41;
DR TrEMBL: P00517; GP41; 1.
FT NON_TER 1
FT TER 1
SEQUENCE 219 AA; 25353 MW; F65829B01520D91 CRC64;
SO Query Match 96.7%; Score 88; DB 15; Length 219;
Best Local Similarity 93.8%; Pred. No. 3,2e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSMCKCKRLVCYTS 16
DB 57 LLSMCKCKRLVCYTS 72

RESULT 3
ID 0807G2 PRELIMINARY; PRT; 890 AA.
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DR ENV polypeptide (fragment).
OC Human immunodeficiency virus type 1.
OS Virus; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
SEQUENCE FROM N.A.
RA Yamauchi Y., Vallat A.S., Swanson P., Bodelle P., Kapur L.,
RT Ngunjiri C., Zekeng L., Gutler L.G., Devere S.G., Brennan C.A.;
RL "Evaluation of HIV Type 1 Group O Isolates: Identification of Five
DR EMBL: AJ236404; CAB96282.1;
DR InterPro: IPR000328; ENV_GP41;
DR TrEMBL: P00517; GP41; 1.
FT NON_TER 1
FT TER 1
SEQUENCE 890 AA; 100610 MW; BBE816CC6C45E23 CRC64;
SO Query Match 96.7%; Score 89; DB 15; Length 890;
Best Local Similarity 93.8%; Pred. No. 1,3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSMCKCKRLVCYTS 16
DB 620 LLSMCKCKRLVCYTS 635

RESULT 4
OY1855
AC 0918B6 PRELIMINARY; PRT; 218 AA.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

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DB GP41 (fragment).
OS ENV.
OS Human immunodeficiency virus type 1.
OC Virus; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
SEQUENCE FROM N.A.
RA Robert P., Robertson D., Sandrine S., Christel D., Francois S.,
RT Philippe M.;
RL "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
DR EMBL: AJ236404; CAB96282.1;
DR InterPro: IPR000328; ENV_GP41;
DR TrEMBL: P00517; GP41; 1.
FT NON_TER 1
FT TER 1
SEQUENCE 218 AA; 25243 MW; E7F0B2E0F79FA8 CRC64;
SO Query Match 95.6%; Score 87; DB 15; Length 218;
Best Local Similarity 87.5%; Pred. No. 4,7e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSMCKCKRLVCYTS 16
DB 54 LLSMCKCKRLVCYTS 69

RESULT 5
ID 091ED5 PRELIMINARY; PRT; 538 AA.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DR ENV polypeptide (fragment).
OC Human immunodeficiency virus type 1.
OS Virus; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
SEQUENCE FROM N.A.
RA Robert P., Robertson D., Sandrine S., Christel D., Francois S.,
RT Philippe M.;
RL "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
DR EMBL: AJ236404; CAB96282.1;
DR InterPro: IPR000328; ENV_GP41;
DR TrEMBL: P00517; GP41; 1.
FT NON_TER 1
FT TER 1
SEQUENCE 538 AA; 60777 MW; B3C956A233FE1D CRC64;
SO Query Match 95.6%; Score 87; DB 15; Length 538;
Best Local Similarity 87.5%; Pred. No. 1,2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSMCKCKRLVCYTS 16
DB 374 LLSMCKCKRLVCYTS 389

RESULT 6
OY1855
AC 0918B6 PRELIMINARY; PRT; 219 AA.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

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DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DR Sp1 (fragment).
CR 544 (fragment).
OC Human immunodeficiency virus type 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Philippe M., Robertson D., Sandrine S., Francois S.,
RL "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
EMBL AJ236391; CB96240.1; -.
DR InterPro: IPR000328; ENV_Gp41.
PF pfam: PF00517; GP41; 1.
KM Transmembrane. 1
FT NON_TER 219 219
SQ SEQUENCE 219 AA; 25363 MW; 85C2DC5B5F528907 CRC64;

Query Match 94.4%; Score 86; DB 15; Length 219;
Best Local Similarity 87.5%; Pred. No. 7,1e-07;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 L15SGCKGRALVCYTS 16
DB 56 L15SGCKGRALVCYTS 71

RESULT 7
Q91HU9 PRELIMINARY; PRT; 130 AA.
ID Q91HU9
AC Q91HU9
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DR 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Envelope glycoprotein (fragment).
GN GP41.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=2038675; PubMed=10933623;
RA Yang C., Gao F., Fongjuno P.N., Zekeng L., van der Groen G.,
RA Plenzak D., Schable C., Lai R.B.;
RA Phylogenetic analysis of protease and transmembrane regions of HIV
RA AIDS Reg Hum. Retroviruses 16:1075-1081(2000).
DR EMBL: AF229235; AAF71912.1; -.
DR InterPro: IPR000328; ENV_Gp41.
PF pfam: PF00517; GP41; 1.
KM Transmembrane.
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 15393 MW; 5385789A33644A CRC64;

Query Match 93.4%; Score 85; DB 15; Length 130;
Best Local Similarity 87.5%; Pred. No. 6,2e-07;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 L15SGCKGRALVCYTS 16
DB 40 L15SGCKGRALVCYTS 55

RESULT 8
Q91ECT PRELIMINARY; PRT; 216 AA.
ID Q91ECT
AC Q91ECT
DT 01-OCT-2000 (TREMBLrel. 15, Created)

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DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DR Sp1 (fragment).
CR 544 (fragment).
OC Human immunodeficiency virus type 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Philippe M., Robertson D., Sandrine S., Francois S.,
RL "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
EMBL AJ236392; CB96241.1; -.
DR InterPro: IPR000328; ENV_Gp41.
PF pfam: PF00517; GP41; 1.
KM Transmembrane. 1
FT NON_TER 216 216
SQ SEQUENCE 216 AA; 25015 MW; 780C5F39CA6997C2 CRC64;

Query Match 93.4%; Score 85; DB 15; Length 216;
Best Local Similarity 93.8%; Pred. No. 1e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 L15SGCKGRALVCYTS 16
DB 55 L15SGCKGRALVCYTS 70

RESULT 9
Q91EP2 PRELIMINARY; PRT; 535 AA.
ID Q91EP2
AC Q91EP2
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DR 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Env polypeptide (fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BCF03;
RA Roques P., Brun-Vezinet F., Domet P.,
RA Delpech M.,
RA HIV-1 group O phylogenetic analysis of C2-GP41 region."
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
EMBL AJ13055; CB96216.1; -.
DR InterPro: IPR000328; ENV_Gp41.
DR InterPro: IPR000777; GP130.
PF pfam: PF00516; GP120; 1.
DR EMBL: AF229235; AAF71912.1; -.
DR AIDS; Coat protein, Glycoprotein, Polypeptide, Transmembrane.
FT NON_TER 535 535
SQ SEQUENCE 535 AA; 59682 MW; 7234B89780D12C5 CRC64;

Query Match 93.4%; Score 85; DB 15; Length 535;
Best Local Similarity 93.8%; Pred. No. 2,6e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 L15SGCKGRALVCYTS 16
DB 374 L15SGCKGRALVCYTS 389

RESULT 10
Q807H0 PRELIMINARY; PRT; 872 AA.
ID Q807H0
AC Q807H0
DT 01-OCT-2000 (TREMBLrel. 15, Created)

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DT 01-JUN-2002 (TREMBLER). 21. Created)
DT 01-JUN-2002 (TREMBLER). 21. Last sequence update)
RC Envelope glycoprotein.
DE Envelope glycoprotein.
GN ENV.
CC Human immunodeficiency virus type 1.
CV NCB1_TaxID=11676;
RM
RP SEQUENCE FROM N.A.
RC STRAIN=98CM4453;
MEDLINE=21849375; PubMed=11860674;
Yamauchi U., Vallari A.S., Swanson P., Bodelle P., Kapteue L.,
Nganop C., Zekeng L., Guttler L.G., Devare S.G., Brennan C.A.;
"Evaluation of HIV Type 1 Group O Isolates: Identification of Five
Phylogenetic Clusters."
RT AIDS Res. Hum. Retroviruses 18:269-282(2002).
DR EMBL; AF318325; AL09873.1;
SQ SEQUENCE 872 AA; 98344 MW; 91D37F6005382783 CRC64;
Query Match 93.4%; Score 85; DB 15; Length 872;
Best Local Similarity 87.5%; Pred. No. 4,2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSMCKCKRGLVCTYS 16
DB 602 LLSMCKCKRGLVCTYS 617

RESULT 11
O807F9 PRELIMINARY; PRT; 887 AA.
AC O807F9;
DT 01-JUN-2002 (TREMBLER). 21. Created)
DT 01-JUN-2002 (TREMBLER). 21. Last sequence update)
DE Envelope glycoprotein.
GN ENV.
CC Human immunodeficiency virus type 1.
CV NCB1_TaxID=11676;
RM
RP SEQUENCE FROM N.A.
RC STRAIN=98CM4453;
MEDLINE=21849375; PubMed=11860674;
Yamauchi U., Vallari A.S., Swanson P., Bodelle P., Kapteue L.,
Nganop C., Zekeng L., Guttler L.G., Devare S.G., Brennan C.A.;
"Evaluation of HIV Type 1 Group O Isolates: Identification of Five
Phylogenetic Clusters."
RT AIDS Res. Hum. Retroviruses 18:269-282(2002).
DR EMBL; AF318325; AL09873.1;
SQ SEQUENCE 882 AA; 99193 MW; 627BCA5D0C90564 CRC64;
Query Match 93.4%; Score 85; DB 15; Length 882;
Best Local Similarity 87.5%; Pred. No. 4,2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSMCKCKRGLVCTYS 16
DB 613 LLSMCKCKRGLVCTYS 628

RESULT 12
O807H6 PRELIMINARY; PRT; 887 AA.
AC O807H6;
DT 01-JUN-2002 (TREMBLER). 21. Created)
DT 01-JUN-2002 (TREMBLER). 21. Last sequence update)
DE Envelope glycoprotein.
GN ENV.
CC Human immunodeficiency virus type 1.
CV NCB1_TaxID=11676;
RM
RP SEQUENCE FROM N.A.
RC STRAIN=SP-M1321;
MEDLINE=20584646; PubMed=11153079;
Ortiz M., Munoz L., Bernal A., Rodriguez A., Zorruguino A.,
Vinales, Retroviral Virens, Retroviridae; Lentivirus.

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OX NCB1_TaxID=11676;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=98CM4124;
MEDLINE=21849375; PubMed=11860674;
Yamauchi U., Vallari A.S., Swanson P., Bodelle P., Kapteue L.,
Nganop C., Zekeng L., Guttler L.G., Devare S.G., Brennan C.A.;
"Evaluation of HIV Type 1 Group O Isolates: Identification of Five
Phylogenetic Clusters."
RT AIDS Res. Hum. Retroviruses 18:269-282(2002).
DR EMBL; AF318325; AL09873.1;
SQ SEQUENCE 887 AA; 99366 MW; E210F13F7B2474D CRC64;
Query Match 93.4%; Score 85; DB 15; Length 887;
Best Local Similarity 87.5%; Pred. No. 4,2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSMCKCKRGLVCTYS 16
DB 618 LLSMCKCKRGLVCTYS 633

RESULT 13
O807G9 PRELIMINARY; PRT; 887 AA.
AC O807G9;
DT 01-JUN-2002 (TREMBLER). 21. Created)
DT 01-JUN-2002 (TREMBLER). 21. Last sequence update)
DE Envelope glycoprotein.
GN ENV.
CC Human immunodeficiency virus type 1.
CV NCB1_TaxID=11676;
RM
RP SEQUENCE FROM N.A.
RC STRAIN=98CM4453;
MEDLINE=21849375; PubMed=11860674;
Yamauchi U., Vallari A.S., Swanson P., Bodelle P., Kapteue L.,
Nganop C., Zekeng L., Guttler L.G., Devare S.G., Brennan C.A.;
"Evaluation of HIV Type 1 Group O Isolates: Identification of Five
Phylogenetic Clusters."
RT AIDS Res. Hum. Retroviruses 18:269-282(2002).
DR EMBL; AF318325; AL09873.1;
SQ SEQUENCE 887 AA; 99595 MW; 88954F4ED76A314A CRC64;
Query Match 93.4%; Score 85; DB 15; Length 887;
Best Local Similarity 87.5%; Pred. No. 4,2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLSMCKCKRGLVCTYS 16
DB 618 LLSMCKCKRGLVCTYS 633

RESULT 14
O807J9 PRELIMINARY; PRT; 135 AA.
AC O807J9;
DT 01-JUN-2002 (TREMBLER). 16. Created)
DT 01-MAR-2001 (TREMBLER). 16. Last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
CC Human immunodeficiency virus type 1.
CV NCB1_TaxID=11676;
RM
RP SEQUENCE FROM N.A.
RC STRAIN=SP-M1321;
MEDLINE=20584646; PubMed=11153079;
Ortiz M., Munoz L., Bernal A., Rodriguez A., Zorruguino A.,
Vinales, Retroviral Virens, Retroviridae; Lentivirus.

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